

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:41:32 ; Search time 34.65 Seconds
(without alignments)
1600.893 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSCIISLFTFAV.....RSYPEILTLKTYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	5019	100.0	915	17 AAR86596	A2058 autotaxin pr
2	5019	100.0	915	22 AAY71987	Human melanoma aut
3	4681	93.3	863	22 AAY71988	Human teratocarcin
4	4632	92.3	859	22 AAY71991	Human autotaxin pr
5	4533	90.3	829	17 AAR86578	Autotaxin derived
6	4430.5	88.3	858	22 AAY71997	Rat autotaxin vari
7	4430.5	88.3	858	22 AAY71999	Rat autotaxin vari
8	4429.5	88.3	858	22 AAY71998	Rat autotaxin vari
9	4426.5	88.2	858	22 AAY71986	Rat autotaxin prot
10	4423.5	88.1	858	22 AAY71996	Rat autotaxin vari
11	4422.5	88.1	858	22 AAY71995	Rat autotaxin vari

12	4341	86.5	849	17 AAR86595	N-tera 2D1 autotax
13	4306	85.8	885	22 AAY71989	Rat brain autotaxi
14	4279	85.3	979	17 AAR86580	Autotaxin derived
15	3842	76.5	788	17 AAR86579	Autotaxin derived
16	1955.5	39.0	873	21 AAY83620	Human PC-1 polypep
17	1955.5	39.0	925	16 AAR79148	Human insulin rece
18	1955.5	39.0	925	20 AAY39355	Insulin receptor t
19	1955.5	39.0	925	21 AAB00195	Breast cancer prot
20	1954.5	38.9	873	21 AAY83621	Variant human PC-1
21	646.5	12.9	457	21 AAG31321	Arabidopsis thalia
22	609	12.1	461	21 AAG29474	Arabidopsis thalia
23	609	12.1	465	21 AAG29473	Arabidopsis thalia
24	599	11.9	400	21 AAG29475	Arabidopsis thalia
25	569	11.3	359	21 AAG31322	Arabidopsis thalia
26	512	10.2	453	20 AAY17529	Human secreted pro
27	512	10.2	453	20 AAY02378	Polypeptide identi
28	512	10.2	453	22 AAB90545	Human secreted pro
29	484	9.6	338	21 AAG31323	Arabidopsis thalia
30	467	9.3	440	21 AAB18910	A novel polypeptid
31	465.5	9.3	477	21 AAB24072	Human PRO1107 prot
32	465.5	9.3	477	21 AAY66716	Membrane-bound pro
33	465.5	9.3	477	22 AAB65239	Human PRO1107 (UNQ
34	465	9.3	411	20 AAY34445	Porphorymonas ging
35	465	9.3	428	20 AAY34324	Porphorymonas ging
36	360	7.2	438	21 AAW90962	Human CSGP-2 prote
37	357	7.1	355	19 AAW75859	Human secretory pr
38	357	7.1	355	20 AAY45165	Human secreted pro
39	241.5	4.8	133	21 AAG31319	Arabidopsis thalia
40	200	4.0	92	21 AAG31320	Arabidopsis thalia
41	179	3.6	109	19 AAW52839	Secreted protein e
42	141	2.8	39	21 AAB53540	Human colon cancer
43	134	2.7	111	13 AAR26050	MSF-K130. Synthet
44	134	2.7	182	12 AAR10872	Protein encoded by
45	134	2.7	452	16 AAR80041	Human megakaryocyt

ALIGNMENTS

RESULT 1

AAR86596

ID AAR86596 standard; Protein; 915 AA.

XX

AC AAR86596;

XX

DT 01-JUL-1996 (first entry)

XX

DE A2058 autotaxin protein.

XX

XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;

KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO9532221-A2.

XX

PD 30-NOV-1995.

XX

PF 24-MAY-1995; 95WO-US06613.

XX

PR 28-NOV-1994; 94US-0346455.

XX

PR 25-MAY-1994; 94US-0249182.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Krutzch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX

DR WPI; 1996-020533/02.

XX

PT Autotaxin motility stimulating protein, and DNA encoding it - used
in cancer diagnosis and therapy

XX

PS Claim 4; Page 91-94; 112pp; English.

Good data

CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.

XX	SQ	Sequence	915 AA;
Query Match 100.0%; Score 5019; DB 22; Length 915; Best Local Similarity 100.0%; Pred. No. 0; Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MARRSSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK	60
Db	1	marrssfqcqiisltfavgvsiiclgftahrikraegweegpptvlsdspwtnisgsk	60
QY	61	GRCFELQEAAGPPDCRDNLCKSVTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC	120
Db	61	grcfelqeagppdcrcdnlcksvtscchdfdelclktargwectkrcgevrneenachc	120
QY	121	SEDCCLARGDCCTNYQVCKGESHVDDDCCEEIKAAECPAGFVRPPLIIFSVDFRASVMK	180
Db	121	sedclargdcctnyqvckgeshvdddceeikaaecpagfvrpplifsvdfrasymk	180
QY	181	KGSKVMPNIEKLKRCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFA	240
Db	181	kgskvmpnieklrscgthspymrpvyptktpnlytlatgtypeshgivgnsmydpvfa	240
QY	241	TFHLRGREKFNHRWGGQPLWTATKQGVKAGTFFWSVIPHERILTLRLWTLPLDHER	300
Db	241	tfhlrgrekfnhrwggqplwtatkqgvkagtfffwsvipherriltlrlwtlpldher	300
QY	301	PSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPFTPAKRPRKRVAPKRQERPVAAPPKRRR	360
Db	301	psvyafyseqpdfsgkhkygpfpgpeessygsftpakrprkvapkrqerpvaappkrrr	360
QY	361	KIHRMDHYAAETQDKMTNPLREIDKIVGQMDGLKQLKRRCVNVIFVGDHGMEDVTCD	420
Db	361	kihrmdhyaaetrqdkmntplreidkivgqlmdglkqlkrrcvnvifvgdhgmedvtcd	420
QY	421	RTEFLSNYLTNVDDITLVPGLGRIRSKFSNNAKYDPKAIANLTCKKPDQHFKPYLKQH	480
Db	421	rteflsnyltnvdditlvpgtlgrirskfsnnakypdkaiianltckkpdqhfkpylkqh	480
QY	481	LPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVE	540
Db	481	lpkrlhyannrriedihllverrrwhvarkpldvyykpsgkcfqgdhgfndknvsmqtvf	540
QY	541	VGYGPTFKYKTKVPPFENTIELYNVCMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV	600
Db	541	vgygptfkyktkvpfenielynvmcdllgkbpapnngthgslnhlrltntfrptmpeev	600
QY	601	TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGSPEERHLLYGRPAVLVRT	660
Db	601	trpnypgimylsqdfdlgctcddkvepknkldelnkrlhtkgspeerhlllygrpavlyrt	660
QY	661	RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCL	720
Db	661	rydilyhtdfesgyseifmlmlwtsytvskqaevsvpdhltscvrpdvrvspfsqncl	720
QY	721	AYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRLVKKYASER	780
Db	721	aykndkmsygfllppylssspeakydaflvtnmvpmpyafkrvwnyfqrvlvkkyaser	780
QY	781	NGNVISGPIFDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSLDFTQPADKCDGP	840
Db	781	ngnvvisgpifdydydglhdtedkikqyvegssipvpthyysiiitsclftqpadkcdgp	840
QY	841	LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE	900
Db	841	lsvssfllphrpdneescnsdeskwveelkmhtarvrdiehltsldffrktsrsype	900
QY	901	ILTLKTYLHTYSEI 915	
Db	901	iltlktylhtyesei 915	

RESULT 3			
AA71988			
ID	AA71988	standard; Protein; 863 AA.	
XX	AA71988;		
AC	AA71988;		
XX	28-MAR-2001	(first entry)	
DT	28-MAR-2001	(first entry)	
XX	Human teratocarcinoma autotaxin.		
DE	Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;		
XX	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;		
KW	therapy; metabolic disease; obesity; dyslipidemia; serum glucose;		
KW	non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;		
KW	type I phosphodiesterase activity; ATP pyrophosphatase activity;		
KW	ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.		
XX	Homo sapiens.		
OS			
XX			
FH	Key	Location/Qualifiers	
FT	Binding-site	127..129	
FT		/label= RGD_binding_domain	
FT	Active-site	201..213	
FT		/note= "Autotaxin phosphodiesterase catalytic site"	
XX	WO200068386-A1.		
PN	16-NOV-2000.		
PD			
XX	05-MAY-2000; 2000WO-US12402.		
PF			
XX	07-MAY-1999; 99US-0306979.		
PR	(ZYMO) ZYMOGENETICS INC.		
XX	Kelly JD;		
PI	WPI; 2001-007397/01.		
XX	New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -		
PT	Claim 27; Page 108-110; 126pp; English.		
PS			
XX	The present sequence is autotaxin isolated from human teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.		
XX	Sequence	863 AA;	
SQ			

Query Match 93.3%; Score 4681; DB 22; Length 863; Best Local Similarity 93.8%; Pred. NO. 0; Matches 858; Conservative 2; Mismatches 3; Indels 52; Gaps 1;			
QY	1	MARRSSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK	60
Db	1	marrssfqcqiisltfavgvniclgftahrikraegweegpptvlsdspwtnisgsk	60

QY	61	GRCFELQEA	PPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNERNACHC	120
Db	61	grcfelqeag	ppdcrcdnlcksytsccdhdfelclktarawectkdrcevnrneenachc	120
QY	121	SEDCLARGDC	TNYQVVCKGESHVWDDCEIEKAAECPAGFVRPPLIIFSVDGFRASYMK	180
Db	121	sedclargdc	tnyqvvcckgeshwdddceiekaaecpagfvrppliifsvdgrfasymk	180
QY	181	KGSKVMPNIE	KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNMSYDVPVFDA	240
Db	181	kgskvmpnie	klrscgthspymrpvyptktpfnlytlatgлыпeshgivgnmsydpvfda	240
QY	241	TFHLRGREKE	FNHRWGGQPLWITATKQGVKAGTEFFWSVIPHERRLITILRWLTLPDHER	300
Db	241	tfhlrgrekn	hrwggqplwitatkqgvkagtfwsvvipherrilitilrgwltlpdher	300
QY	301	PSVYAFYSE	QDPFSGHKYGPFGPEESSYSGSPPTPAKRPRKRVAPKRRQRPVAPPKRRR	360
Db	301	psvyafyse	qdpfsgghkygpgfe-----	324
QY	361	KIHRMDHYA	ETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCNVIVFGDHGMEDVTCD	420
Db	325	-----	-----mtnplreidkivgqlmdglkqlkhrvcnvivfgdhgmedvtcd	368
QY	421	RTEFLSNYL	TNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIANLTCKKPDQHFKPYLKQH	480
Db	369	rteflsnyl	tnvdditlvpgtglgrirskfsnnakydpkaianltckkpdqhfkyplkqh	428
QY	481	LPKRLHYAN	NRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVP	540
Db	429	lpkrlhyann	rriedihllverrwvharkpldvyykpsgkcfqgdhgfndknvsmqtvf	488
QY	541	VGYGPTFKY	TKVPFPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPPEV	600
Db	489	vgygptfky	tkvkvpffenielynmcdllglkpapnngthgslnhllrtntfrptmpeev	548
QY	601	TRPNYPGIM	YQLQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEEHLLYGRPAVLYRT	660
Db	549	trpnypgim	yqlsqdfdlgctcdkvepknkldelnkrlhtkgsteerhlllygrpavlyrt	608
QY	661	RYDILYHTD	FESGYSEIFIMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVRSFSQNC	720
Db	609	rydilyhtd	fesgyseifimplwtstytvskaevssvpdhltscvrpdvrvsfsqnc	668
QY	721	AYKNDKQMS	YGFLEPPYLSSSPEAKYDAFLVTNMVMPYPAKRVWNYFQRLVKKYASER	780
Db	669	aykndkqms	ygfleppylssspeakydaflvtnmvmpypafkrvwnyfqrvlvkkyaser	728
QY	781	NGNVVISGP	IFDYDYGDLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP	840
Db	729	ngnvvisgp	ifdydydglhdedkikqyvegssipvpthyysitscldftqpadkcdgp	788
QY	841	LSVSSFILP	HRPDNEESCNSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE	900
Db	789	lsvssfилp	hrpdneescnsdeskwveelmkmhtarvrdiehltsldffrktersype	848
QY	901	ILTLKTYLH	TFYSEI 915	
Db	849	iltlkyllh	tyesei 863	
RESULT 4				
AAY71991				
ID	AAY71991 standard; Protein; 859 AA.			
XX				
AC	AAY71991;			
XX				
DT	28-MAR-2001 (first entry)			
XX				
DE	Human autotaxin protein.			
XX				
KW	Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;			
KW	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;			

KW	therapy; metabolic disease; obesity; dyslipidemia; serum glucose;				
KW	non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;				
KW	type I phosphodiesterase activity; ATP pyrophosphatase activity;				
KW	ATPase; adenosine-5'-triphosphatase activity.				
XX	Homo sapiens.				
OS					
XX					
FH	Location/Qualifiers				
FT	Key	Domain	8..26	/note= "Putative transmembrane domain"	
FT	Cleavage-site	44..45			
FT	Binding-site	123..125		/label= RGD_binding_domain	
FT	Active-site	197..209		/note= "Putative phosphodiesterase active site"	
XX	WO200068386-A1.				
PN	16-NOV-2000.				
XX					
PF	05-MAY-2000; 2000WO-US12402.				
XX					
PR	07-MAY-1999; 99US-0306979.				
XX	(ZYMO) ZYMOGENETICS INC.				
PA	Kelly JD;				
XX	WPI; 2001-007397/01.				
DR	N-PSDB; AAD02133.				
XX	New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -				
PPT	Claim 27; Page 119-121; 126pp; English.				
PPT	The present sequence is human autotaxin protein.				
XX	Autotaxin is a glycoprotein cytokine which increases				
CC	insulin signalling in adipose tissue by producing substrate for				
CC	adenosine receptors, resulting in inhibition of lipolysis,				
CC	decreased hepatic gluconeogenesis and serum glucose levels, and				
CC	increased insulin sensitivity. It also inhibits differentiation				
CC	of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5' -				
CC	triphosphatase (ATPase) and ATP pyrophosphatase activities.				
CC	Autotaxin and its analogues are used to stimulate glucose uptake				
CC	by cells, particularly to reduce serum glucose levels for				
CC	treatment of non-insulin dependent diabetes (NIDDM) in humans,				
CC	or generally any condition associated with elevated serum levels				
CC	of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).				
CC	Transgenic animals that overexpress autotaxin are models for				
CC	human metabolic diseases.				
XX	Sequence 859 AA;				
SQ					
Query Match 92.3%; Score 4632; DB 22; Length 859;					
Best Local Similarity 93.7%; Pred. No. 0;					
Matches 848; Conservative 3; Mismatches 2; Indels 52; Gaps					
QY	11	QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGCKGRCFELQEAG	70		
Db	7	riislftfavgvniclgftahrikraegweegpptvlsdspwtnisgckgrcfelqeag	66		
QY	71	PPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHCEDCLARGDC	130		
Db	67	ppdcrcdnlcksytsccchdfdelclktargwectkdrcevnrneenachcsedclargdc	126		
QY	131	CTNYQVVCKGESHVWDDCEIEKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE	190		
Db	127	ctnyqvvckgeshvwdddceiekaaecpagfvrppliifsvdgrfasymkkgskvmpnie	186		
QY	191	KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNMSYDVPVDFATFHLRGREKF	250		

Db 187 klrscgthspmrpyptktnlylatglypeshgivgnsmypvdatfhlgrekf 246

QY 251 NHRWGGQPLWITATKQGVKAGTFFWSVWIPHERRILTLRWLTLPDHERPSVYAFYSEQ 310

Db 247 nhrwggqplwitatkgvkgagtffwsvvipherriltilqlwltlpdherpsvyafyseq 306

QY 311 PDFSGHKYGPFGPEESSYGSPTPAKRPRKRVAPKRRQERPAPPKRRRKIHRMDHYAA 370

Db 307 pdfsgkhygpgpe----- 320

QY 371 ETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLT 430

Db 321 -----mtnplreidkivgqlmdgkqlklhrcvnvifvgdhgmedvtcdrtfslsnylt 374

QY 431 NVDDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANN 490

Db 375 nvdditlvpgtlgrirskfsnnakydpkaiianltckkpdqghfkpylkqhlpkrlhyann 434

QY 491 RRIEDIHLLVERRWHVARKPLDVYKKPSGKCFEQGDHGFNDKVNMQTVFVGYGPTFKYK 550

Db 435 rriedihllverwhvarkpldvyykpsgkcfqgdhgfndkvnsmqtvfvygypftfkyk 494

QY 551 TKVPPFENIELYNVCMDDLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMY 610

Db 495 tkvppfenielynvmcdllgkpapnngthgslnhllrtntfrptmpeeetrpnypgimy 554

QY 611 LQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEEHLLYGRPAVLYRTRYDILYHTDF 670

Db 555 lqsdfdlgctcddkvepknkldelnkrlhtkgsteerhllgrpavlyrtrydilyhtdf 614

QY 671 ESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCLAYKNDKQMSY 730

Db 615 esgyseiflmlplwtsytsvskgaevsvpdhltscvrpdvrsvpsfsqncLAYkndkqmsy 674

QY 731 GFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRLVKKYASERNGVNVISGPI 790

Db 675 gflfppylssspeakydafivtnmvpmpyafkrvwnyfqrlvkkyaserngvnvvisgpi 734

QY 791 FDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPH 850

Db 735 fdydydglhdtedkikqyvegssipvpthyysiltsclfdtqpadkcdgplsvssfilph 794

QY 851 RPDNEESCNSSEDESKVVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTlKTYLHT 910

Db 795 rpdneescnsdeskvwveelmkmhtarvrdiehltsldfrktsrsypeilTLtktylht 854

QY 911 YESEI 915

Db 855 yesei 859

RESULT 5

AAR86578

ID AAR86578 standard; Protein; 829 AA.

XX

AC AAR86578;

XX

DT 28-JUN-1996 (first entry)

XX

DE Autotaxin derived from melanoma cell line A2058.

XX

XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;

KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO9532221-A2.

XX

PD 30-NOV-1995.

XX

PF 24-MAY-1995; 95WO-US06613.

XX

PR 28-NOV-1994; 94US-0346455.

PR 25-MAY-1994; 94US-0249182.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Krutzech J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX

DR WPI; 1996-020533/02.

DR N-PSDB; TO6612.

XX

PT Autotaxin motility stimulating protein, and DNA encoding it - used

PT in cancer diagnosis and therapy

XX

PS Claim 4; Page 57-60; 112pp; English.

XX

CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is

CC an autocrine motility stimulating protein which is present in cancer

CC cells. ATX stimulates both random and directed migration of melanoma

CC cells. The tumorous form of ATX is a secreted protein, while the

CC transmembrane bound form is not present in tumour cells. The cDNA

CC encoding this sequence can be used in a vector, to transform cells. The

CC recombinant cells can then be used to produce the peptide sequences.

CC Antibodies specific for these sequences can be produced, and can be used

CC in cancer diagnosis and therapy. Different sites of localisation of the

CC protein are utilised for diagnosis and prognosis of the stages of tumour

CC progression. The sequences can be used in treatment methods to

CC advantageously block the activity of the secreted form of ATX, while

CC having little effect on the membrane form of AXT.

XX

SQ Sequence 829 AA;

Query Match 90.3%; Score 4533; DB 17; Length 829;

Best Local Similarity 99.9%; Pred. NO. 0;

Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECKDRCGEVNRNEENACHCSEDCIARGDCCTNYQVVKGESHWVD 146

Db 1 chdfdelclktargweckdrcevrneenachsedclargdcctnyqvckgeshwvd 60

QY 147 DDCEEIKAAECPAGEFVRPPLIIFSVDFRASVMKKGSKVMPNIEKLRSCGTHSPMRPVY 206

Db 61 ddceeikaaecpagfvrpplifsvdgrasvmkkgskvmpnieklrscgthspmrpv 120

QY 207 PTKTFPNLYTLATGLYPESHGIVGNMYPVDFATFHLRGREKFNHRWGGQPLWITATK 266

Db 121 ptktfpnlytlatglypeshgivgnsmypvdfatfhlgrekfnhrwggqplwitatk 180

QY 267 QGVKAGTFFWSVIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 326

Db 181 qgvkagtfwsvvipherriltilrwltlpdherpsvyafyseqpdfsghkygpgfpees 240

QY 327 SYGSPFTPAKRPRKRVAPKRRQERPAPPKRRRKIHRMDHYAAETRQDKMTNPLREIDK 386

Db 241 sygsptpakrprkvapkrqrerpappkrrrkihrmthyaaetrqdkmntplreidk 300

QY 387 IVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGLGRIR 446

Db 301 ivgqlmdgkqlklrcvnvifvgdhgmedvtcdrtfslsnyltnvdditlvpgtlgrir 360

QY 447 SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVERRWHV 506

Db 361 skfsnnakydpkaiianltckkpdqghfkpylkqhlpkrlhyannrriedihlverwhv 420

QY 507 ARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVFVGYGPTFKYKTKVPPFENIELYNVCM 566

Db 421 arkpldvyykpsgkcfqgdhgfndkvnsmqtvfvygptfkyktkvppfenielynvmc 480

QY 567 DLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYLQSDFDLGCTCDDKVE 626

Db 481 dllglkpapnngthgslnhllrtntfrptmpeeetrpnypgimylqsdldlgctcddkve 540

QY 627 PKNKLDLNLKRLHTKGSTEEHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 686

Db 541 pknkidelnrlhtkgssteerhlllygrpavlyrtrydilyhtdfesgyselfmlmlwtsy 600

QY 687 TVSKOAEVSSVPDHLTSCVRPDVRVSPFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKY 746

Db 601 tvskgaeivssvpdhltscvrpdvrsvpsfsqncLAYKNDKQMSYGFLFPPYLSSSPEAKY 660

QY 747 DAFLVTNMPVMPYPAFKRVWNYFORVLVKYASERNGVNVISGPIFDYDGLHDTEDKIK 806

Db 661 dafivtmvmpypafkrwnyqrvlrvkkyaserngvnisgpifdydydglhdtedkik 720

QY 807 QYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPNNEESCNSSSEDESK 866

Db 721 qyvegssipvpthyysiiTSCldftqpadkcdgplsvssfilphrpdneescnsdesk 780

QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 915

Db 781 wveelmkmtarvrdiehltsldffrktsrsypeiltlktylhtyesei 829

RESULT 6

AAY71997

ID AAY71997 standard; Protein; 858 AA.

XX

AC AAY71997;

XX

DT 28-MAR-2001 (first entry)

XX

DE Rat autotaxin variant (S236T).

XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;

KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;

KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;

KW type I phosphodiesterase activity; ATP pyrophosphatase activity;

KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.

XX

OS Rattus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 236

FT /note= "Wild type Ser substituted by Thr"

XX

PN WO200068386-A1.

XX

PD 16-NOV-2000.

XX

PF 05-MAY-2000; 2000WO-US12402.

XX

PR 07-MAY-1999; 99US-0306979.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Kelly JD;

XX

DR WPI; 2001-007397/01.

XX

PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and

PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX

PS Disclosure; Page -: 126pp; English.

XX

CC The present sequence is variant (S236T) of rat autotaxin protein.

CC Autotaxin is a glycoprotein cytokine which increases insulin

CC signalling in adipose tissue by producing substrate for adenosine

CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin

CC sensitivity. It also inhibits differentiation of adipocytes.

CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase

CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its

CC analogues are used to stimulate glucose uptake by cells, particularly

CC to reduce serum glucose levels for treatment of non-insulin dependent

CC diabetes (NIDDM) in humans, or generally any condition associated

CC with elevated serum levels of glucose, lipid or free fatty acid

CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress

CC autotaxin are models for human metabolic diseases.

CC Note: The present sequence is not shown in the specification

CC but is derived from rat autotaxin protein sequence found in

CC page 101-104 of sequence listing (AAY71986).

XX

SQ Sequence 858 AA;

Query Match 88.3%; Score 4430.5; DB 22; Length 858;

Best Local Similarity 88.7%; Pred. No. 0;

Matches 803; Conservative 30; Mismatches 19; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGCKGRCFELQEAG 70

Db 7 rvislftfaisvniclglftasikrae-wdegpptvlsdswptntsgsckgrcfelgev 65

QY 71 PDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHCEDCLARGDC 130

Db 66 pdcrcdnlcksyssccchdfdelclktargwectkdrogevrneenachcedclsrgec 125

QY 131 CTNYQVVCKGESHWVDDCEEIKAAECFAGFVRPPLIIFSDGFRASYMKKSKVMPNIE 190

Db 126 ctnyqvvcckgeshwvddceeiKvpecpagfvrpplifsvdgrasymkkgskvmpnie 185

QY 191 KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKF 250

Db 186 klrscgthapymrpvyptktpnlytlatgлыпeshgivgnsmydpvdfatfhlrgrekf 245

QY 251 NHRWGGQPLWITATKQGVKAGTFEWSVVIPIHERRILTLRLWLTPDHERPSVYAFYSEQ 310

Db 246 nhrwggqplwitatkqgvragtfwsvsipherriltilqlwslpdrnerpsvafyseq 305

QY 311 PDFSGHKYGPFGPEESSYSGSPFPAKRPKRKVAPKRRQRPVAPPKRRRKIHRMDHYAA 370

Db 306 pdfsghkygpfge----- 319

QY 371 ETRQDKMTNPLREIDKIVQQLMDGLKQLKLRRCNVIVFGDHGMEDVTCDRTEFLSNYLT 430

Db 320 -----mtnplreidktvgqlmdglikqlrhrcvnmvifvgdhgmedvtcdrtfslnyt 373

QY 431 NVDDITLVPGTGLRIRSKFSNNAKYDPAKAIANLTCKKPDQHFYKYLKQHLPKRLHYANN 490

Db 374 nvdditlvpgtglriraksinnksydkptliantlckkpdqhfkympkqhlpkrlhyann 433

QY 491 RRIEDIHLLVERRRWHVARKPLDVYKPSGCKFFQGDHGFNDKVNMQTVFVGYGPTFKYK 550

Db 434 rriedihllvdrrwhvarkpldvyykpsgkcfqgdhgfndknvsmqtvfvygptfkyr 493

QY 551 TKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRLTRNTFRTPMPEEVRPNYPGIMY 610

Db 494 tkvppfenielynmvcdllglkpapngthgslnhllrtntfrtptmpdevsrpnypgimy 553

QY 611 LQSEFDLGCCTDDKVEPKNKDELNKLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDF 670

Db 554 lqsefdlgctcddkvepknkleeInklhtkgsteerhlllygrpavlyrtsydylyhtdf 613

QY 671 ESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCLAYKNDKQMSY 730

Db 614 esgyseiflmpwlwtsytiskgaevssipehltncvrvpsvpsqncLAYKNDKQMSY 673

QY 731 GFLFPPYLSSSPEAKYDAFLVTNMPVMPYPAFKRVWNYFORVLVKYASERNGVNVISGPI 790

Db 674 gflfppylssspeakydaflvtnmvmpypafkrvwayfgrvlvkkyaserngvnisgpi 733

QY 791 FDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPH 850

Db 734 fdnydglrdtedeikqyvegssipvpthyysiiTSCldftqpadkcdgplsvssfilph 793

QY 851 RPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHT 910

Db 794 rpdnescnsdesedskwveelmkmtarvrdiehlTgldfyrktsrsyseiltlktylht 853

XX Rat autotaxin variant (R265K).

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;

KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;

KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;

KW type I phosphodiesterase activity; ATP pyrophosphatase activity;

KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.

XX

OS Rattus sp.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Misc-difference 265

FT /note= "Wild type Arg substituted by Lys"

XX

XX WO200068386-A1.

PN

XX 16-NOV-2000.

PD

XX

XX 05-MAY-2000; 2000WO-US12402.

PF

XX

XX 07-MAY-1999; 99US-0306979.

PR

XX (ZYMO) ZYMOGENETICS INC.

PA

XX Kelly JD;

PI

XX

XX WPI; 2001-007397/01.

DR

XX

PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and

PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX

PS Disclosure; Page -; 126pp; English.

XX

CC The present sequence is variant (R265K) of rat autotaxin protein.

CC Autotaxin is a glycoprotein cytokine which increases insulin

CC signalling in adipose tissue by producing substrate for adenosine

CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin

CC sensitivity. It also inhibits differentiation of adipocytes.

CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase

CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its

CC analogues are used to stimulate glucose uptake by cells, particularly

CC to reduce serum glucose levels for treatment of non-insulin dependent

CC diabetes (NIDDM) in humans, or generally any condition associated

CC with elevated serum levels of glucose, lipid or free fatty acid

CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress

CC autotaxin are models for human metabolic diseases.

CC Note: The present sequence is not shown in the specification

CC but is derived from rat autotaxin protein sequence found in

CC page 101-104 of sequence listing (AA71986).

XX

SQ Sequence 858 AA;

Query Match 88.3%; Score 4429.5; DB 22; Length 858;

Best Local Similarity 88.7%; Pred. No. 0;

Matches 803; Conservative 30; Mismatches 19; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGSICLGFTAHRIKRAEGWEEGPTVLSDSPWTNISGCKGRCFELQAG 70

Db :|||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |

7 rvislftfaisvniclgftasrikrae-wdegptvlstdspwtntsgskgrcfelqevg 65

QY 71 PPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDKRCGEVRNEENACHCSECLARGDC 130

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

66 ppdcrcdnlcksysccchdfdelclkrtargweckdkrcgevrneenachcsedclsrge 125

QY 131 CTNYQVVKGESHWDDCEIEKAAECAPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE 190

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

126 ctnyqvckgeshwvddcceikvpecpagfvrpplifsvdgdfrasmkkgskvmpnie 185

QY 191 KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKF 250

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

186 klrscgthapymrpvyptkftfnlytlatglypeshigivgnsmydpvdfasfhlrgrekf 245

QY 251 NHRWGGQPLWITATKQGVKAGTFWVWIPHERRILITILRWLTLPDHERPSVYAFYSEQ 310

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

246 nhrwggqplwitatkqgvkagtfwsvsipherriltlwlslpdrnerpsvyafyse 305

QY 311 PDFSGHKYGPFGPEESSYSGPFTPAKRPKRKVAPKRRQERPVPAPPKRRRKIHRMDHYAA 370

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

306 pdfsghkygpfge----- 319

QY 371 ETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCNVNIFVGDHGMEDVTCDRTEFLSNYLT 430

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

320 ----mtnplreidktvgqlmdglkqlrhrcvnnvifvgdhgmedvtcdrtfslsnyt 373

QY 431 NVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANN 490

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

374 nvdditlvpgtlgriraksinnskydpktianltckkpdqhfkpykmqhlpkrlhyann 433

QY 491 RRIEDIHLLVERRHWVARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVFVGYPFTFKYK 550

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

434 rriedihllvdrwhvarkpldvyykpsgkcfqgdhgfndknvsmqtvfvgypftfkyr 493

QY 551 TKVPPFENIELYNVCMCDLLGLKPAPNNGTHGSLNHLRLTNTFRTPMPEEVRTPNYPGIMY 610

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

494 tkvppfenielynmvcmcdllglkpapnngthgslnhlrltntfrtptmpdevsrpnypgimy 553

QY 611 LQSFEDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDF 670

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

554 lqsfedlgctcddkvepknkleeinkrlhtkgsteerhlllygrpavlyrtsydilyhtdf 613

QY 671 ESGYSEIFLMLLWTSYTVSKQAEVSSVDPDHLTSCVRPDVRSVSPSONCLAYKNDKQMSY 730

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

614 esgyseiflmlwtsytiskgaeysvipehltnvcvrdvrvspgfsqncldaykndkqmsy 673

QY 731 GLFPPYLSSSPEAKYDAFLVTNMPVMPYPAKRVWNYFQRLVLYKKYASERNGVNVISGPI 790

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

674 glfppylssspeakydafvltnmvmypafkrvwayfqrvlvkkyaserngvnvvisgpi 733

QY 791 FDYDYGDLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPH 850

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

734 fdynydgldrtdedeikqyvegssipvpthyysiiitscldftqpackcdgplsvssfilph 793

QY 851 RPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTFRSRYPEILTLKTYLHT 910

Db |||||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

794 rpdndescnsseideskwveelmkmhtarvrddiehltgldfyrktsrsyseiltlktylht 853

QY 911 YESEI 915

Db ||||| yesei 858

RESULT 9

AA71986

ID AAY71986 standard; Protein; 858 AA.

XX

AC AAY71986;

XX

DT 28-MAR-2001 (first entry)

XX

DE Rat autotaxin protein.

XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;

KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;

KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;

KW type I phosphodiesterase activity; ATP pyrophosphatase activity;

KW ATPase; adenosine-5'-triphosphatase activity.

XX

OS Rattus sp.

XX

PH Key Location/Qualifiers

FT Misc-difference 194 /note= "Wild type Ala substituted by Val"
XX
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
XX WPI; 2001-007397/01.
DR
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Disclosure; Page -; 126pp; English.
XX
CC The present sequence is variant (A194V) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic
CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 88.1%; Score 4423.5; DB 22; Length 858;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 802; Conservative 30; Mismatches 20; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGCKGRGFELQEAG 70
:|||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
Db 7 rvislftfaisvniclgftasrikrae-wdegpptvlspdwtntsgsckgrcfelqevg 65

QY 71 PPDCRCNDLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHCSEDCLARGDC 130
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 66 ppdccrcndlcksyscchdfdelclktargwectkrcgevrneenachcsedclsrqdc 125

QY 131 CTNYQVVCKGESHVDDDCCEEIKAAECFAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE 190
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 126 ctnyqvvckgeshvdddcceeikvpcpagfvrppliifsvdgfrasymkkgskvmpnie 185

QY 191 KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKF 250
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 186 klrscgthpymrpvyptktfnpnlytlatglypeshgivgnsmydpvdfasflhrgrekf 245

QY 251 NHRWWGGQPLWITATKQGVKAGTFFWSVVPHERRILTLRWLTLPDHERPSVYAFYSEQ 310
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 246 nhrwwggqplwitatkqgvragtffwsvsipheririlqlwslpdpnerpsvayfyseq 305

QY 311 PDFSGHKYGFPGPEESSYGSPTTAKRPRKRKVAPKRRQERPVPAPKRRRKIRHMDHYAA 370
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 306 pdfsghkygpgpe----- 319

QY 371 ETRQDKMTNPLREIDKIVQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLT 430
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|

Db 320 -----mtnplreidktvgqlmdglkqlrlhrcvnnvifvgdhgmedvtcdrtfslsnylt 373
QY 431 NVDDITLVPCTGLGRIRSKFSNNAKYDPAKAIANLTCKKKPDQHPKPYLKQHLPKRLHYANN 490
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 374 nvdditlvpgtllgriraksinnskydptkiiianltckkpdqhfkympmkqhlprlhyann 433
QY 491 RRIEDIHLLVERRHWARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVFVGYPTEFKYK 550
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 434 rriedihllvdrwhvarkpldvyykkpsgkcfqgdhgfndkvnsmqtvfvgypgptfkyr 493
QY 551 TKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMY 610
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 494 tkvppfenielynvmcdllglkpapnngthgslnhlrltntfrptmpdevsrpnypgimy 553
QY 611 LQSDFDLGCTCDDKVEPKNKLDENKRLHTKGSTEEHLLYGRPAVLRYTRYDILYHTDF 670
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 554 lqsefalgctcddkvepknkleeinkrlhtkgsteerhlllygrpavlyrtsydilyhtdf 613
QY 671 ESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSY 730
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 614 esgyseiflmlplwtsytiskqaeavssipehltncvrpdvrvspgfsqncclaykndkqmsy 673
QY 731 GFLRPPYLSSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRLVLVKKYASERNGVNVISGPI 790
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 674 gflfpylssspeakydaflvtnmvmypafkrvwayfqrvlvkkyaserngvnvisgpi 733
QY 791 FDYDYGDLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPH 850
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 734 fdynydgldrtdedeikqyvegsslpvpthyysiitscldftqpadkcdgplsvssfilph 793
QY 851 RPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSSYPEILTLKTYLHT 910
|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|
Db 794 rpdndescnsdesedskwveelmkmhtarvrddiehltgldfyrktsrseyseiltktylht 853
QY 911 YESEI 915
|||||
Db 854 yesei 858

RESULT 11
AAY71995
ID AAY71995 standard; Protein; 858 AA.
XX
AC AAY71995;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (A93V).
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 93 /note= "Wild type Ala substituted by Val"
FT
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX

CC sequences can be used in treatment methods to advantageously block the
CC activity of the secreted form of AXT, while having little effect on the
CC membrane form of AXT.

XX SQ Sequence 849 AA;

Query Match 86.5%; Score 4341; DB 17; Length 849;
Best Local Similarity 87.9%; Pred. No. 0;
Matches 811; Conservative 11; Mismatches 19; Indels 82; Gaps 7;

QY 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60
|||||
Db 1 marrssfqcqisllftfavgvniclgftahrikraegweegpptvlsdspwnisgsck 60
|||||
QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFELCLKTARGWECTKDRCGEVRNEENACHC 120
|||||
Db 61 grcfelqeagppdcrcdnlcksytsccchdfelclktarawectkdrcevrneenachc 120
|||||
QY 121 SEDCLARGDCTNYQVVKGESHWVDDCEETKAAECPAGFVRPPLIIFSVDGFRASYMK 180
|||||
Db 121 sedclargdctnyqvckgeshwvddceetkaaecpagfvrppliifsvdgfrasymk 180
|||||
QY 181 KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
|||||
Db 181 kgskvmpnieklrscgthshmrpvpyptktfnplytlatglypeshgivgnsmydvpfda 240
|||||
QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWSVVI---PHERRILTLRWLTLP 296
|||||
Db 241 tfhlrgrekfnhrwggqplwitatkrges---wnllvcchpsraeiltilqwtlp 296
|||||
QY 297 DHER----PSVYAFYSEQPDFSGHKYGFPGPESSYGSPTPAKRPRKRVAPKRRQRPV 352
|||||
Db 297 dherlrmpsilsl- ----isldtnmpfgpe----- 323
|||||
QY 353 APPKKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKRRCVNVIFVGDH 412
|||||
Db 324 -----mtnplreidkivgqlmdgkqlklhrcvnmvifvgdh 359
|||||
QY 413 GMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQH 472
|||||
Db 360 gmedvtcdrteflsnlyltnvdditlvpgtlg-irskfsnnakypkaianltckkpdqh 418
|||||
QY 473 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGCKFFQGDHGFDNK 532
|||||
Db 419 fkpylkqhlpkrlhyannrrriedihllverrvharkpldvyykpsgckffqgdhgfdnk 478
|||||
QY 533 VNSMQTVFVGYPFTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTF 592
|||||
Db 479 vnsmtqvfvgypftfkytkvppfenielynmcdllglkpnngthgslnhlrrtnf 538
|||||
QY 593 RPTMPEEVRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKRHLTKGSTERHLLYG 652
|||||
Db 539 rptmpeevrpnypgimylsqdfdlgctcddkvepknkldelnkrlhtkgsteerhllyg 598
|||||
QY 653 RPAVLYRTRYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDVRVS 712
||
Db 599 rp-----htdfesgyseiflmpwtstyskqaevsvpdhltsvrvpdvrvs 646
|||||
QY 713 PSFSQNCLAYKNDQMSYGFLEPPYLSSSPEAKYDAFLVTNMVMPYPAKRVNMFQRVL 772
|||||
Db 647 psfsqncalaykndqmsygfleppylssspeakydaflvtnmvmypafkrvnmfqrvl 706
|||||
QY 773 VKKYASERNGVNVISGPIFDYDYGDLHDTEDTKIQYVEGSSIPVPTHYYSIITSLDFTQ 832
|||||
Db 707 vkkyaserngvnvisgpifdydylhdtedkikqyvegssipvpthyysiitsclldftq 766
|||||
QY 833 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 892
|||||
Db 767 padkcdgplsvssfilrhrpdneescnsdeskvwveelmkmhtarvrdiehltsldffr 826
|||||
QY 893 KTSRSYPEILTLKTYLHTYESEI 915
|||||

Db 827 ktsrsypeiltlktylhtyesei 849

RESULT 13
AAY71989
ID AAY71989 standard; Protein; 885 AA.
XX
AC AAY71989;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat brain autotaxin designated as PD-Ialpha.
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; PD-Ialpha; brain;
KW nucleotide pyrophosphatase.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Binding-site 126..128
FT /label= RGD_binding_domain
FT Region 591..615
FT /note= "This region is absent in rat autotaxin
FT sequence (AAY71986)"
PN WO200068386-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Claim 27; Page 110-113; 126pp; English.
XX
CC The present sequence is autotaxin isolated from rat brain tissue.
CC This sequence is designated as nucleotide pyrophosphatase
CC (PD-Ialpha). Autotaxin is a glycoprotein cytokine increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic
CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
XX
SQ Sequence 885 AA;

Query Match 85.8%; Score 4306; DB 22; Length 885;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

QY 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60

Db 1 marrsfqseqdislftfavgvniclgtfahrikraegweegpptvldspwtnisgck 60
Qy 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHC 120
Db 61 grcfelqeagppdcrcdnlcksytsccchdfdelclktarawectkdrcevrneenachc 120
Qy 121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEEIKAAECAPAGFVRPPLIIFSVDGF--RASY 178
Db 121 sedclargdctnyqvvckgeshvwdcceeeikaaecqlq--vcspsinhlirgwlpmtsy 178
Qy 179 MKKGSKVMPIEKLRCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF 238
Db 179 mkkgskvmpnieklrcscgthspymrpvyptktfnpnlytlatgtypeshgivgnsmydpvf 238
Qy 239 DATFHLRGREKFNHRWVGQPLWITATKQGVKAGTFFWSVVI-----PHERRILTLRWLT 294
Db 239 datfhlrgrekfnhrwvggqplwitatkrges----wnllvcchpsraeiltilqwt 294
Qy 295 LPDHERPSYAFYSEQPDFSGHKYGPFGPEESSYSGSPFPAKRPKRKVAPKRRQERPVP 354
Db 295 lpdherpsvyafyseqpdfsgkhkmpfge----- 324
Qy 355 PKKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGM 414
Db 325 -----mtnplremhkivgqlmdgklqlkhlrcvvnvifv---et 359
Qy 415 EDVTCD--RTEFLSNLYTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKKPDQH 472
Db 360 mdgrchmyrteflsnlytnvdditlvpgltrirskfsnnakypkaiianltckkpdqh 419
Qy 473 FKPYLKQHLPKRLHYANNRRIEDIHLLVERRHWARKPLDVYKKPSGKCFQGDHGFDNK 532
Db 420 fkpylkqlpkrlhyannrriedihllverrhwarkpldvyykkpsgnafsrrettafkn 479
Qy 533 VNSMOTVFVGYPTEFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTE 592
Db 480 vnsmtvfvgygptfkyytkvppfenielynmcdllglkpapnngthgslnlhrtntf 539
Qy 593 RPTMPEEVRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLKNKRLHTKSGSTEERHLLYG 652
Db 540 rptmpeevrpnypgimylqsdfdlgctcdckvepknkldelnkrlhtkgsteerhllyg 599
Qy 653 -RPAVLYRIRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV 711
Db 600 drpavlyrtrydilyhtdfesgyseiflmlplwtsytvskqaevsvpdhltscvrpdvr 659
Qy 712 SPFSQNCIAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPFAKRVWNYFQRV 771
Db 660 spfsqnciaykndkmsyglfppylssspeakydaflvtnmvpmpafkrvwnyfqrv 719
Qy 772 LVKKYASERNGVNVISGPIFDYDYGDLHDTEDIKQYVEGSSIPVPTHYYSIITSCLDFT 831
Db 720 lvkkyaserngvnvisgpifdydydglhdtedkikgyvegssipvpthyysiltsclft 779
Qy 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF 891
Db 780 qpakcdgplsvssfilphrpdneescnsdeskweelmkmhtarvrdiehltsldff 839
Qy 892 RKTSRSYPEILTLKTYLHTYSEI 915
Db 840 rktsrsypeiltlktylhtyesei 863
RESULT 15
AAR86579
ID AAR86579 standard; Protein; 788 AA.
XX
AC AAR86579;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin derived from teratocarcinoma N-tera 2D1 cells.
XX

KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
OS Homo sapiens.
XX
PN WO9532221-A2.
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US066613.
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX
DR WPI; 1996-020533/02.
DR N-PSDB; AAT06613.
XX
PT Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
XX
PS Claim 4; Page 62-65; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of AXT, while
CC having little effect on the membrane form of AXT.
XX
SQ Sequence 788 AA;

Query Match 76.5%; Score 3842; DB 17; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

Qy 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNRNEENACHSEDCLARGDCCTNYQ 135
Db 1 cdnlcksytscchdfdelclktarawectkdrcevrneenachsedclargdcctnyq 60
Qy 136 VVCKGESHVWDDCEEEIKAAECAPAGFVRPPLIIFSVDGF--RASVMKKGSKVMPIEKL 193
Db 61 vvckgeshwddcceeeikaaecqlq--vdspsinhlirgwlpmtsymkkgskvmpniekl 118
Qy 194 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHR 253
Db 119 scgthspymrpvyptktfnpnlytlatgtypeshgivgnsmydpvdfatfhlrgrekfnhr 178
Qy 254 WVGGOPLWITATKQGVKAGTFFWSVVI---PHERRILTLRWLTLPDHERPSYAFYSE 309
Db 179 wwagqplwitatkrges---wnllvcchpsraeiltilqwtlpdherpsvyafyse 234
Qy 310 QPDFSGHKYGPFGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPKRRRKIHRMDHYA 369
Db 235 qpdfsgkhkmpfge----- 249
Qy 370 AETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD--RTEFLSN 427
Db 250 -----mpnplremhkivgqlmdgklqlkhlrcvvnvifv---etmdgrchmyrteflsn 299
Qy 428 YLTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFAPYLKQHLPKRLHY 487

Db 300 yltnvdditlvpgtlgrirskfssnakdydpkaiaianltckkpdqghfkpylkqhlpkrlhy 359

QY 488 ANNRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKNVNSMQTVFVGYPGF 547

Db 360 annrriedihllverrwvharkpldykkpsgnafsrrettafdnkvnsmqtvfvgypgf 419

QY 548 KYTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPG 607

Db 420 kytkvppfenielynvmcdllgkpapnngthfslnhllrtntfrptmpeevtrpnypg 479

QY 608 IMYQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG-RPAVLYRTRYDILY 666

Db 480 imylqsdfdlgctcddkvepknkldelnkrlhtkgsteerhlllygdrpavlyrtrydily 539

QY 667 HTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDK 726

Db 540 htdfesgyseiflmlwtsytvskqaevsvpdhltscvrpdrvrvpsfsqncclaykndk 599

QY 727 QMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAPFKRVWNYFORVLVKKYASERNGVNVI 786

Db 600 qmsygglgppylssspeakydaflvtnmvpmpafkrvwnyfqrvlvkkyaserngvnvi 659

QY 787 SGPIFDYDYDGLHDEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF 846

Db 660 sgpifdydydglhdedkikqyvegssipvpthyysiitsclldftqpadkcdgplsvssf 719

QY 847 ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKT 906

Db 720 ilphrpdneescnssedekwveelnmhtarvrdiehltsldffrktssrsypeiltlkt 779

QY 907 YLHTYESEI 915

Db 780 ylhtyesei 788

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:42:27 ; Search time 20.45 Seconds
(without alignments)
901.337 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSCQIISLFFAV.....RSYPEILTLKTLVHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1	US-08-346-455B-69
2	5019	100.0	915	3	US-08-977-221-69
3	5019	100.0	915	5	PCT-US95-06613-69
4	4533	90.3	829	1	US-08-346-455B-34
5	4533	90.3	829	3	US-08-977-221-34
6	4533	90.3	829	5	PCT-US95-06613-34
7	4418	88.0	861	1	US-08-346-455B-67
8	4418	88.0	861	3	US-08-977-221-67
9	4418	88.0	861	5	PCT-US95-06613-67
10	4279	85.3	979	1	US-08-346-455B-38
11	4279	85.3	979	3	US-08-977-221-38
12	4279	85.3	979	5	PCT-US95-06613-38
13	3842	76.5	788	1	US-08-346-455B-36
14	3842	76.5	788	3	US-08-977-221-36
15	3842	76.5	788	5	PCT-US95-06613-36
16	1955.5	39.0	873	3	US-09-187-331-6
17	1955.5	39.0	925	2	US-08-392-946-1
18	1955.5	39.0	925	2	US-08-504-169-1
19	1955.5	39.0	925	5	PCT-US94-14893-1
20	360	7.2	438	3	US-09-187-331-2
21	357	7.1	355	2	US-09-014-969-19
22	192	3.8	39	1	US-08-346-455B-54
23	192	3.8	39	3	US-08-977-221-54
24	192	3.8	39	5	PCT-US95-06613-54
25	126.5	2.5	2471	4	US-09-112-450-4
26	123	2.5	4654	4	US-08-476-515A-84
27	123	2.5	4655	4	US-08-652-877-84

28	123	2.5	4655	4	US-08-652-877-88	Sequence 88, Appl
29	123	2.5	4655	4	US-08-652-877-90	Sequence 90, Appl
30	122	2.4	4655	4	US-08-652-877-86	Sequence 86, Appl
31	118	2.4	23	1	US-07-822-043-11	Sequence 11, Appl
32	115	2.3	1833	3	US-08-479-722B-2	Sequence 2, Appli
33	115	2.3	1833	5	PCT-US95-02251-18	Sequence 18, Appl
34	113	2.3	22	1	US-07-822-043-33	Sequence 33, Appl
35	113	2.3	22	1	US-08-346-455B-33	Sequence 33, Appl
36	113	2.3	22	3	US-08-977-221-33	Sequence 33, Appl
37	113	2.3	22	5	PCT-US95-06613-33	Sequence 33, Appl
38	112	2.2	1394	6	5177197-30	Patent No. 5177197
39	110	2.2	23	1	US-08-346-455B-11	Sequence 11, Appl
40	110	2.2	23	3	US-08-977-221-11	Sequence 11, Appl
41	110	2.2	23	5	PCT-US95-06613-11	Sequence 11, Appl
42	109.5	2.2	1810	5	PCT-US95-11684-4	Sequence 4, Appli
43	108	2.2	465	3	US-08-701-582D-13	Sequence 13, Appl
44	108	2.2	465	3	US-09-063-893A-19	Sequence 19, Appl
45	107.5	2.1	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-346-455B-69
; Sequence 69, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOFILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA

; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-346-455B-69

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSSFQSCQIIISLFTFAVGVSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db 1 MARRSSFQSCQIIISLFTFAVGVSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60

QY 61 GRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
Db 61 GRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVVKGESHVWDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCCTNYQVVKGESHVWDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180

QY 181 KGSKVMPIEKLRSCTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLRSCTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240

QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300

QY 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFTPAKPRKVKAPKRRQERPVPAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFTPAKPRKVKAPKRRQERPVPAPPKRRR 360

QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKLRRCNVIVFGDHGMEDVTC 420
Db 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKLRRCNVIVFGDHGMEDVTC 420

QY 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPAKAIANLTCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPAKAIANLTCKKPDQHFKPYLKQH 480

QY 481 LPKRLHYANNRRIEDIHLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540

QY 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600

QY 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGRPAVLRYT 660
Db 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGRPAVLRYT 660

QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVSPFSQNC 720

QY 721 AYKNDKQMSYGFLFPYLSSSPEAKYDAFLVTNMVMPYPAKRVWNYFQRLVKKYASER 780
Db 721 AYKNDKQMSYGFLFPYLSSSPEAKYDAFLVTNMVMPYPAKRVWNYFQRLVKKYASER 780

QY 781 NGNVVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGNVVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGP 840

QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRYPE 900
Db 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRYPE 900

QY 901 ILTLKTYLHTESEI 915
Db 901 ILTLKTYLHTESEI 915

RESULT 2
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69

Query Match 100.0%; Score 5019; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSSFQSCQIIISLFTFAVGVSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db 1 MARRSSFQSCQIIISLFTFAVGVSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60

QY 61 GRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120

Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECFAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECFAGFVRPPLIIFSVDGFRASYMK 180
QY 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPPKRRR 360
QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRCVNVIFVDHGMEDVTCD 420
Db 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRCVNVIFVDHGMEDVTCD 420
QY 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAILANLTCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAILANLTCKKPDQHFKPYLKQH 480
QY 481 LPKRLHYANNRRIEDIHLVERRHHVARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVERRHHVARKPLDVYKKPSGKCFQGDHGFNDKNVSMQTVF 540
QY 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
QY 601 TRPNYPGIMYLSDFDLGCTCDDKVEPKNKLDLNLKRLHRTKGSTEERHLLYGRPAVLRYT 660
Db 601 TRPNYPGIMYLSDFDLGCTCDDKVEPKNKLDLNLKRLHRTKGSTEERHLLYGRPAVLRYT 660
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSFSONCL 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSFSONCL 720
QY 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAKRVWNYFQRLVKKYASER 780
Db 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAKRVWNYFQRLVKKYASER 780
QY 781 NGNVVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYISITSLDFTQPADKCDGP 840
Db 781 NGNVVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYISITSLDFTQPADKCDGP 840
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900
Db 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900
QY 901 ILTLKTYLHTYESEI 915
Db 901 ILTLKTYLHTYESEI 915

RESULT 3
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PCT-US95-06613-69

Query Match 100.0%; Score 5019; DB 5; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60
QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECFAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECFAGFVRPPLIIFSVDGFRASYMK 180
QY 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERILLTILRWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPPKRRR 360

Db 421 ARKPLDVYKKPSGKFFQGDHGFNDKNVNSMQTVFVGYPTEFKYKTKVPPFENIELYNVMC 480
QY 567 DLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYQSDFDLGCTCDDKVE 626
Db 481 DLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYQSDDDLCTCDDKVE 540
QY 627 PKNKLDLKNKRLHTKGSSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTSY 686
Db 541 PKNKLDLKNKRLHTKGSSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTSY 600
QY 687 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPPYLSSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPPYLSSSSPEAKY 660
QY 747 DAFLVNTNMPMPYPAFKRVWNYFQRLVKKKYASERNGVNVISGPIFDYDYGDLHDTEDKIK 806
Db 661 DAFLVNTNMPMPYPAFKRVWNYFQRLVKKKYASERNGVNVISGPIFDYDYGDLHDTEDKIK 720
QY 807 QYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 866
Db 721 QYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 780
QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 829
RESULT 5
US-08-977-221-34
; Sequence 34, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34
Query Match 90.3%; Score 4533; DB 3; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 87 CHDFDELCLKTARGWECKDRCGEVRNEENACHCEDCLARGDCCTNYQVVCKGESHWD 146
Db 1 CHDFDELCLKTARGWECKDRCGEVRNEENACHCEDCLARGDCCTNYQVVCKGESHWD 60
QY 147 DCEEIKAAECPAGFVRPPLIFSVDFGRASYMKKSGKVMNPNIKLRSCGTHSPYMRPVY 206
Db 61 DCEEIKAAECPAGFVRPPLIFSVDFGRASYMKKSGKVMNPNIKLRSCGTHSPYMRPVY 120
QY 207 PTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGQPLWITATK 266
Db 121 PTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGQPLWITATK 180
QY 267 QGVKAGTFFWSVIPHERRILTLRWLTLPDHERPSYAFYSEQPDFSGHKYGPFGPEES 326
Db 181 QGVKAGTFFWSVIPHERRILTLRWLTLPDHERPSYAFYSEQPDFSGHKYGPFGPEES 240
QY 327 SYGSPFPAKRPKRKVAPKRRQRPVAPPKRRRKIHRMDHYAAETQDKMTNPLREIDK 386
Db 241 SYGSPFPAKRPKRKVAPKRRQRPVAPPKRRRKIHRMDHYAAETQDKMTNPLREIDK 300
QY 387 IVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGLGRIR 446
Db 301 IVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGLGRIR 360
QY 447 SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVRRWHV 506
Db 361 SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVRRWHV 420
QY 507 ARKPLDVYKKPSGKCFQGDHGFNDKNVNSMQTVFVGYPTEFKYKTKVPPFENIELYNVMC 566
Db 421 ARKPLDVYKKPSGKCFQGDHGFNDKNVNSMQTVFVGYPTEFKYKTKVPPFENIELYNVMC 480
QY 567 DLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYQSDFDLGCTCDDKVE 626
Db 481 DLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYQSDDDLCTCDDKVE 540
QY 627 PKNKLDLKNKRLHTKGSSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTSY 686
Db 541 PKNKLDLKNKRLHTKGSSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTSY 600
QY 687 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPPYLSSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPPYLSSSSPEAKY 660
QY 747 DAFLVNTNMPMPYPAFKRVWNYFQRLVKKKYASERNGVNVISGPIFDYDYGDLHDTEDKIK 806

Db 661 DAFLVTNMVMPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 720
QY 807 QYVEGSSIPVPHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 866
Db 721 QYVEGSSIPVPHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 780
QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 829

RESULT 6
PCT-US95-06613-34
; Sequence 34, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:

; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34

Query Match 90.3%; Score 4533; DB 5; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECTKDRCGEVRNEENACHCEDCLARGDCCTNYQVVCKGESHWVD 146
Db 1 CHDFDELCLKTARGWECTKDRCGEVRNEENACHCEDCLARGDCCTNYQVVCKGESHWVD 60

QY 147 DDCETKAAECPAGFVRPPLIIFSVDFRASVMKKGSKVMPNIEKLRSCGTHSPYMRPVY 206
Db 61 DDCETKAAECPAGFVRPPLIIFSVDFRASVMKKGSKVMPNIEKLRSCGTHSPYMRPVY 120

QY 207 PTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFDATFHLRGREKFNHRWVGQPLWITATK 266
Db 121 PTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFDATFHLRGREKFNHRWVGQPLWITATK 180

QY 267 QGVKAGTFWSVWIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGFPGPEES 326
Db 181 QGVKAGTFWSVWIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGFPGPEES 240

QY 327 SYGSPFTPAKRPRKRVAPKRRQERPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 386
Db 241 SYGSPFTPAKRPRKRVAPKRRQERPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 300

QY 387 IVQLMDGLKQLKLRRCNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR 446
Db 301 IVQLMDGLKQLKLRRCNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR 360

QY 447 SKFSNNAKYDPKAIIANLTCKKPDQHEKPYLKQHLPKRLHYANNRRIEDIHLVERWHV 506
Db 361 SKFSNNAKYDPKAIIANLTCKKPDQHEKPYLKQHLPKRLHYANNRRIEDIHLVERWHV 420

QY 507 ARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGPTFKYKTKVPPFENIELYNVVC 566
Db 421 ARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGPTFKYKTKVPPFENIELYNVVC 480

QY 567 DLLGLKPAPNNGTHGSLNHLRLTRNTFRPTMPEEVRPNYPGIMYLOSDFDLCTCDDKVE 626
Db 481 DLLGLKPAPNNGTHGSLNHLRLTRNTFRPTMPEEVRPNYPGIMYLOSDFDLCTCDDKVE 540

QY 627 PKNKLDLNLKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 686
Db 541 PKNKLDLNLKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 600

QY 687 TVSKQAEVSSVPDHLTSCVRPDVRVSPSQNCLAYKNDKQMSYGFLLPPYLSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDVRVSPSQNCLAYKNDKQMSYGFLLPPYLSSSPEAKY 660

QY 747 DAFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 806
Db 661 DAFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 720

QY 807 QYVEGSSIPVPHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 866
Db 721 QYVEGSSIPVPHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK 780

QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 829

RESULT 7
US-08-346-455B-67
; Sequence 67, Application US/08346455B

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149053
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-67

Query Match 88.0%; Score 4418; DB 3; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

1 MARRSSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTSGSCK 60
1 MARRSSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTSGSCK 60
61 GRCFELQAGPDCRCDNLCKSYTSCCHDFDELCLKTARAWECTKRCGEVRNEENACHC 120
61 GRCFELQAGPDCRCDNLCKSYTSCCHDFDELCLKTARAWECTKRCGEVRNEENACHC 120
121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECPAGEVVRPPLIIFSVVDGFRASYMK 180
121 SEDCLARGDCCTNYQVVCKGESHVWDDCEEIKAAECPAGEVVRPPLIIFSVVDGFRASYMK 180
181 KGSKVMPIEKLRCSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
181 KGSKVMPIEKLRCSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWVSVI---PHERRILTLRLWLTLP 296
241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWVSVI---PHERRILTLRLWLTLP 296
297 DHER----PSVYAFYSEQPDFSGHKYGPFGPESSYGSPTPAKRPKRKVAPKRQERPV 352
297 DHERLRMSPSILSNL-----ISLDTNMPFGPE----- 323
353 APPKRRRKIRHMDHYAAETRQDKMTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDH 412
324 -----MTNPLREIDKIVQGLMDGLKQLKLRRCVNVIFVGDH 359
413 GMEDVTCDRTEFLSNLYTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQH 472
360 GMEDVTCDRTEFLSNLYTNVDDITLVPGTLG-IRSKFSNNAKYDPKAIIANLTCKKPDQH 418

473 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDK 532
419 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDK 478
533 VNSMOTVFVGYGPTFKYKTKVPPFENIELYNVCMDDLGLKPPAPNNGTHGSLNHLRLTNTF 592
479 VNSMOTVFVGYGPTFKYKTKVPPFENIELYNVCMDDLGLKPPAPNNGTHGSLNHLRLTNTF 538
593 RPTMPEEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG 652
539 RPTMPEEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG 598
653 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVDPDHLTSCVRPDVRVS 712
599 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVDPDHLTSCVRPDVRVS 658
713 PSFSQNCCLAYKNDKQMSYGFLEPPYLSSSSPEAKYDAFLVTNMPVMPAFKRVWNYFQFVL 772
659 PSFSQNCCLAYKNDKQMSYGFLEPPYLSSSSPEAKYDAFLVTNMPVMPAFKRVWNYFQFVL 718
773 VKYASERNGVNVISGPIFDYDGLDHTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQ 832
719 VKYASERNGVNVISGPIFDYDGLDHTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQ 778
833 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFR 892
779 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVDRDIEHLTSLDFFR 838
893 KTSRYPEILTLKTYLHTYESEI 915
839 KTSRYPEILTLKTYLHTYESEI 861
RESULT 9
PCT-US95-06613-67
Sequence 67, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434

```

; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: N-tera 2D1 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US95-06613-67

Query Match 88.0%; Score 4418; DB 5; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

QY 1 MARRSFQSCQIISLFTFAVGVSICLGFTHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
Db 1 MARRSFQSCQIISLFTFAVGVSICLGFTHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60

QY 61 GRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCEGEVRNEENACHC 120
Db 61 GRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARAWECTKDRCEGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVCKGESHVWDDCEEIKAAECPAGFVRPPLIIFSVDFGRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVWDDCEEIKAAECPAGFVRPPLIIFSVDFGRASYMK 180

QY 181 KGSKVMPIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240

QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVI---PHERRILTLRWLTLP 296
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGES-----WNILLVCCHPRAEILTILQWLTL 296

QY 297 DHER-----PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPETPAKRPKRKVAPKRRQRPV 352
Db 297 DHERLSMPSILSNL-----ISLDTNMPFGPE----- 323

QY 353 APPKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVQLMDGLKQLKLRRCNVIVFGDH 412
Db 324 -----MTNPLREIDKIVQLMDGLKQLKLRRCNVIVFGDH 359

QY 413 GMEDVTCDRTEFLSNLYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIILANTCKKPDQH 472
Db 360 GMEDVTCDRTEFLSNLYLTNVDDITLVPGTLG-IRSKFSNNAKYDPKAIILANTCKKPDQH 418

QY 473 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDK 532
Db 419 FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDK 478

QY 533 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLHLLRTNTF 592
Db 479 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLHLLRTNTF 538

QY 593 RPTMPEEVRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHFKGSTEERHLLYG 652
Db 539 RPTMPEEVRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHFKGSTEERHLLYG 598

QY 653 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVDPDHLTSCVRPDRVS 712
Db 599 RPAVLYRTRYDVLVYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSSVDPDHLTSCVRPDRVS 658

QY 713 PSFSQNCCLAYKNDKQMSYGFLLFPYLSSSPEAKYDAFLVTNMPVMPAFKRVWNYFQRLV 772
```

```

Db 659 PSFSQNCCLAYKNDKQMSYGFLLFPYLSSSPEAKYDAFLVTNMPVMPAFKRVWNYFQRLV 718
QY 773 VKKYASERNGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQ 832
Db 719 VKKYASERNGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQ 778
QY 833 PADKCDGPLSVSSFILPHRPDNEESNSESSESKWVEELMKMHTARVRDIEHLTSLDFFR 892
Db 779 PADKCDGPLSVSSFILPHRPDNEESNSESSESKWVEELMKMHTARVRDIEHLTSLDFFR 838
QY 893 KTSRSYPEILTLKTYLHTYESEI 915
Db 839 KTSRSYPEILTLKTYLHTYESEI 861

RESULT 10
US-08-346-455B-38
; Sequence 38, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: .PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
```

TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-346-455B-38

Query Match 85.3%; Score 4279; DB 1; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSSFQSCQIIISLFTFAVGVSICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db 1 MARRSSFQSCQDISLFTFAVGVNICLGFTHAHRKRAEGWEEGPTVLSDSPWTNIGSCK 60
QY 61 GRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNNEENACHC 120
Db 61 GRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARAWECTKDRCGEVNNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHWVDDCEIEKAECGAGFVRPPLIIFSVDGF--RASV 178
Db 121 SEDCLARGDCCTNYQVCKGESHWVDDCEIEKAECIQ--VCSPSINHLLRGLPMTSY 178
QY 179 MKKGSKVMPIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF 238
Db 179 MKKGSKVMPIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF 238
QY 239 DATFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVVI-----PHERRILTLRWLT 294
Db 239 DATFHLRGREKFNHRWGGQPLWITATKORGES-----WNILLVCCHPRAEILTILQWLT 294
QY 295 LPDHERPSVYAFYSEQDPFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQERPVP 354
Db 295 LPDHERPSVYAFYSEQDPFSGHKHMPFGPE----- 324
QY 355 PKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRVCNVIFVGDHGM 414
Db 325 -----MTNPLREMHKIVGQMDGLKQLKLRVCNVIEV---ET 359
QY 415 EDVTCDD--RTEFLSNVLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIANLTCKKPDQH 472
Db 360 MDGRCHMYRTEFLSNVLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIANLTCKKPDQH 419
QY 473 FKPYLKQHLPKRLHYANNRRIEDIHLLVERRRWHVARKPLDVYKKPSGKCFQGDHGFENK 532
Db 420 FKPYLKQHLPKRLHYANNRRIEDIHLLVERRRWHVARKPLDVYKKPSGNAFSRETTAFDNK 479
QY 533 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTF 592
Db 480 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTF 539
QY 593 RPTMPEEVRPNYPGIMYLQSDFDLCTCDDKVEPKNKLDELNKLRLHTKGSTEERHLLYG 652
Db 540 RPTMPEEVRPNYPGIMYLQSDFDLCTCDDKVEPKNKLDELNKLRLHTKGSTEERHLLYG 599
QY 653 -RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTSVKQAEVSSVPDHLTSCVRPDVRV 711
Db 600 DRPAVLYRTRYDILYHTDFESGYSEIFLMLPLWTSYTSVKQAEVSSVPDHLTSCVRPDVRV 659
QY 712 SPFSQNCCLAYKNDKQSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAKRVVNYFQRV 771
Db 660 SPFSQNCCLAYKNDKQSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAKRVVNYFQRV 719
QY 772 LVKKYASERNGVNVTSGPIFDYDGLDHTEDKIKQYVEGSSIPVPTHYYSIITSCLDFT 831
Db 720 LVKKYASERNGVNVTSGPIFDYDGLDHTEDKIKQYVEGSSIPVPTHYYSIITSCLDFT 779

QY 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLSLDF 891
Db 780 QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLSLDF 839
QY 892 RKTSSYPEILTLKTYLHTYESEI 915
Db 840 RKTSSYPEILTLKTYLHTYESEI 863
RESULT 11
US-08-977-221-38
; Sequence 38, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:

IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-977-221-38

Query Match 85.3%; Score 4279; DB 3; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY	1	MARRSFSQSCQIISLFTFAVGVSICLGFTTAHRIKRAEGWEEGPTVLSDSPWNTISGSCK	60
Db	1	MARRSFSQSCQDISLFTFAVGVNICLGFTTAHRIKRAEGWEEGPTVLSDSPWNTISGSCK	60
QY	61	GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCKLTARGWECTKDRCGEVRNEENACHC	120
Db	61	GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCKLTARAWECTKDRCGEVRNEENACHC	120
QY	121	SEDCCLARGDCCTNYQVCKGESHWWDDDCCEEIKAAECAPGVRPPLIIFSVDGF--RASY	178
Db	121	SEDCCLARGDCCTNYQVCKGESHWWDDDCCEEIKAAECIQ--VCSPSINHLLRGWLPMTSY	178
QY	179	MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKFPNLYTLATGLYPESHGIVGNSMYDPVF	238
Db	179	MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKFPNLYTLATGLYPESHGIVGNSMYDPVF	238
QY	239	DATEFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVI---PHERILTILRWLT	294
Db	239	DATEFHLRGREKFNHRWGGQPLWITATKQGES----WNILLVCCHPRAEILTILQWLT	294
QY	295	LPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPFPAKRPKRKVAPKRQRVPAP	354
Db	295	LPDHERPSVYAFYSEQPDFSGHKHMPFGPE-----	324
QY	355	PKKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKRRRCVNVIFVGDHGM	414
Db	325	-----MTNPLRHMHKIVGQLMDGLKQLKLRVCNVIEV---ET	359
QY	415	EDVTCD--RTEFLSNYLTNVDDITLVPGLIRGRSKFSNNAKYDPKAIANLTCKKPDQH	472
Db	360	MDGRCHMYRTEFLSNYLTNVDDITLVPGLIRGRSKFSNNAKYDPKAIANLTCKKPDQH	419
QY	473	FKPYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKKPSGCKFFQGDHGFNDK	532
Db	420	FKPYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKKPSGNAFSRETTAFDNK	479
QY	533	VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTF	592
Db	480	VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTF	539
QY	593	RPTMPEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGSSTEERHLLYG	652
Db	540	RPTMPEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGSSTEERHLLYG	599
QY	653	-RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	711
Db	600	DRPAVLYRTRYDILYHTDFESGYSEIFLPLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	659
QY	712	SPSFSQNCLAYKNDKQMSYGFLFPPYLSSSSPEAKYDAFLVTNMVMPYPAKRVWNYFQRV	771
Db	660	SPSFSQNCLAYKNDKQMSYGFLFPPYLSSSSPEAKYDAFLVTNMVMPYPAKRVWNYFQRV	719
QY	772	LVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIKQYVEGSSIPVPTHYYSIITSLDFT	831
Db	720	LVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIKQYVEGSSIPVPTHYYSIITSLDFT	779
QY	832	QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF	891
Db	780	QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF	839
QY	892	RKTSRSYPEILTLKTYLHTYSEI	915
Db	840	RKTSRSYPEILTLKTYLHTYSEI	863

RESULT 12
PCT-US95-06613-38
; Sequence 38, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotaxin
; OTHER INFORMATION: protein sequence from human liver
PCT-US95-06613-38

Query Match 85.3%; Score 4279; DB 5; Length 979;

Best Local Similarity 87.1%; Pred. No. 0;		Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;	
QY	1	MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTISGSCK	60
Db	1	MARRSSFQSCQDISLFTFAVGVSICLGFTAHRIKRAEGWEEGPTVLSDSPWNTISGSCK	60
QY	61	GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC	120
Db	61	GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC	120
QY	121	SEDCLARGDCCNYQVVKGESHWVDDCEEIKAAECPAGEVVRPPLIIFSVDGF--RAS	178
Db	121	SEDCLARGDCCNYQVVKGESHWVDDCEEIKAAECQLQ--VCSPSINHLLRGLPMTSY	178
QY	179	MKKGSKVMPNIEKLKRLSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF	238
Db	179	MKKGSKVMPNIEKLKRLSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF	238
QY	239	DATFHLRGREKNHRWGGQPLWITATKQGVKAGTFEWSVVI-----PHERRILTLRWLT	294
Db	239	DATFHLRGREKNHRWGGQPLWITATKQGES-----WNILLVCCHPSRAEILTLQWLT	294
QY	295	LPDHERPSVAFYSEQPDFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQRPVAP	354
Db	295	LPDHERPSVAFYSEQPDFSGHKMPFGPE-----	324
QY	355	PKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGOLMDGLKQLKLRRCVNVIFVDHGM	414
Db	325	-----MTNPLREMHKIVGOLMDGLKQLKLRRCVNVIFV--ET	359
QY	415	EDVTCD--RTEFLSNLYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIILNLTCKKPDQH	472
Db	360	MDGRCHMYRTEFLSNLYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIILNLTCKKPDQH	419
QY	473	FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGHGFDNK	532
Db	420	FKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGNAFSRETAFDNK	479
QY	533	VNSMQTVFVGYPGTFKYKTKVPPFENIELYNMCDLGLKPAPNNGTHGSLNHLRTNTF	592
Db	480	VNSMQTVFVGYPGTFKYKTKVPPFENIELYNMCDLGLKPAPNNGTHGSLNHLRTNTF	539
QY	593	RPTMPEEVRPNYPGIMYQSDFDLCTCDDKVEPKNKLDLKNRLHTKSGSTEERHLLYG	652
Db	540	RPTMPEEVRPNYPGIMYQSDFDLCTCDDKVEPKNKLDLKNRLHTKSGSTEERHLLYG	599
QY	653	-RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	711
Db	600	DRPAVLYRTRYDILYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	659
QY	712	SPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPFAKRVWNYFQRV	771
Db	660	SPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPFAKRVWNYFQRV	719
QY	772	LVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIQYVEGSSIPVPTHYYSIITSLDFT	831
Db	720	LVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIQYVEGSSIPVPTHYYSIITSLDFT	779
QY	832	QPADKCDGPLSVSSFILPHRPDNEESCSNSEDKQWVEELMKMHTARVRDIEHLTSLDFF	891
Db	780	QPADKCDGPLSVSSFILPHRPDNEESCSNSEDKQWVEELMKMHTARVRDIEHLTSLDFF	839
QY	892	RKTSRSYPEILTLKTYLHTYESEI	915
Db	840	RKTSRSYPEILTLKTYLHTYESEI	863

RESULT 13
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
US-08-346-455B-36

Query Match 76.5%; Score 3842; DB 1; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHCSEDCLARGDCCTNYQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARAWECTKDRCEVRNEENACHCSEDCLARGDCCTNYQ 60

Db	300	YLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAI	IANLTCKKPDQHF	KPYLKQHLPKRLHY	359		
QY	488	ANRRIEDIHLLVERRHWVARKPLDYKKPSGKCF	FQGDHGF	DNKVN	SMQTVEVGYGPTF 547		
Db	360	ANRRIEDIHLLVERRHWVARKPLDYKKPSGNAF	SRETTAF	DNKVN	SMQTVEVGYGPTF 419		
QY	548	KYTKVPPFENIELYNV	MCDDLGLK	PAPNNGTHGSLNHL	LRTNTFRPTMPEEVTRPNYPG 607		
Db	420	KYTKVPPFENIELYNV	MCDDLGLK	PAPNNGTHFSLNHL	LRTNTFRPTMPEEVTRPNYPG 479		
QY	608	IMYQSDFDLGCTCDDK	VEPKNKLD	ELNKR	LHTKGSTEE	RHLLYG-RPAVLYRTRYDILY 666	
Db	480	IMYQSDFDLGCTCDDK	VEPKNKLD	ELNKR	LHTKGSTEE	RHLLYG-RPAVLYRTRYDILY 539	
QY	667	HTDFESGYSEIFLML	LWTSYTV	SKQAEVSSVP	DHLTSCVRPD	VRVSPFSQNC	LAYKNNDK 726
Db	540	HTDFESGYSEIFLMP	LWTSYTV	SKQAEVSSVP	DHLTSCVRPD	VRVSPFSQNC	LAYKNNDK 599
QY	727	QMSYGFLPPPYLSS	SPEAKYDAFL	TNNVPMYPAF	KRVWNYFOR	VLVKKYAS	ERNGVNVI 786
Db	600	QMSYGGLGPPPYLSS	SPEAKYDAFL	TNNVPMYPAF	KRVWNYFOR	VLVKKYAS	ERNGVNVI 659
QY	787	SGPIFDYDYDGLH	DEDKIKQY	VEGSSIPVPT	HYYSIIT	SCLDFTQ	PADKCDGPLSVSSF 846
Db	660	SGPIFDYDYDGLH	DEDKIKQY	VEGSSIPVPT	HYYSIIT	SCLDFTQ	PADKCDGPLSVSSF 719
QY	847	ILPHRPDNEESC	NSSSEDESKW	VEELMKMHTAR	VRDIEHL	TSLDFF	FRKTSRSYPEILTLKT 906
Db	720	ILPHRPDNEESC	NSSSEDESKW	VEELMKMHTAR	VRDIEHL	TSLDFF	FRKTSRSYPEILTLKT 779
QY	907	YLH	YESEI	915			
Db	780	YLH	YESEI	788			

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:26 ; Search time 20.45 Seconds
(without alignments)
12.806 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	788	1 US-08-346-455B-36	Sequence 36, Appl
2	76	100.0	788	3 US-08-977-221-36	Sequence 36, Appl
3	76	100.0	788	5 PCT-US95-06613-36	Sequence 36, Appl
4	76	100.0	829	1 US-08-346-455B-34	Sequence 34, Appl
5	76	100.0	829	3 US-08-977-221-34	Sequence 34, Appl
6	76	100.0	829	5 PCT-US95-06613-34	Sequence 34, Appl
7	76	100.0	915	1 US-08-346-455B-69	Sequence 69, Appl
8	76	100.0	915	3 US-08-977-221-69	Sequence 69, Appl
9	76	100.0	915	5 PCT-US95-06613-69	Sequence 69, Appl
10	76	100.0	979	1 US-08-346-455B-38	Sequence 38, Appl
11	76	100.0	979	3 US-08-977-221-38	Sequence 38, Appl
12	76	100.0	979	5 PCT-US95-06613-38	Sequence 38, Appl
13	71	93.4	861	1 US-08-346-455B-67	Sequence 67, Appl
14	71	93.4	861	3 US-08-977-221-67	Sequence 67, Appl
15	71	93.4	861	5 PCT-US95-06613-67	Sequence 67, Appl
16	69	90.8	873	3 US-09-187-331-6	Sequence 6, Appli
17	69	90.8	925	2 US-08-392-946-1	Sequence 1, Appli
18	69	90.8	925	2 US-08-504-169-1	Sequence 1, Appli
19	69	90.8	925	5 PCT-US94-14893-1	Sequence 1, Appli
20	40	52.6	203	2 US-08-684-024-8	Sequence 8, Appli
21	40	52.6	203	3 US-09-145-868-8	Sequence 8, Appli
22	40	52.6	205	2 US-08-684-024-1	Sequence 1, Appli
23	40	52.6	205	2 US-08-684-024-6	Sequence 6, Appli
24	40	52.6	205	2 US-08-684-024-7	Sequence 7, Appli
25	40	52.6	205	3 US-09-145-868-1	Sequence 1, Appli
26	40	52.6	205	3 US-09-145-868-6	Sequence 6, Appli
27	40	52.6	205	3 US-09-145-868-7	Sequence 7, Appli

28	38	50.0	438	3 US-09-187-331-2	Sequence 2, Appli
29	37	48.7	49	1 US-07-865-166A-6	Sequence 6, Appli
30	37	48.7	254	2 US-08-207-481-20	Sequence 20, Appl
31	37	48.7	254	5 PCT-US95-02689-20	Sequence 20, Appl
32	37	48.7	264	2 US-08-484-905-120	Sequence 120, App
33	37	48.7	264	3 US-08-481-985B-120	Sequence 120, App
34	37	48.7	264	4 US-08-370-476-120	Sequence 120, App
35	37	48.7	436	1 US-08-080-255-8	Sequence 8, Appli
36	37	48.7	436	4 US-08-465-713-8	Sequence 8, Appli
37	37	48.7	436	5 PCT-US93-05857-8	Sequence 8, Appli
38	37	48.7	3969	4 US-08-061-376-5	Sequence 5, Appli
39	36	47.4	309	3 US-08-969-644-20	Sequence 20, Appl
40	36	47.4	309	4 US-08-444-189-20	Sequence 20, Appl
41	36	47.4	359	2 US-08-560-398-10	Sequence 10, Appl
42	36	47.4	516	4 US-09-201-641-6	Sequence 6, Appli
43	36	47.4	707	1 US-08-528-122-18	Sequence 18, Appl
44	36	47.4	707	5 PCT-US95-11720-18	Sequence 18, Appl
45	36	47.4	750	1 US-08-325-553-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein


```

; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
; US-08-346-455B-36

Query Match 100.0%; Score 76; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
    |||||
Db 126 YMRPVYPTKTFPN 138

RESULT 2
US-08-977-221-36
; Sequence 36, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:

```

```

; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
PCT-US95-06613-36

```

```

Query Match 100.0%; Score 76; DB 5; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YMRPVYPTKTFPN 13
Db 126 YMRPVYPTKTFPN 138

```

```

RESULT 4
US-08-346-455B-34
; Sequence 34, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182

```

```

; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-346-455B-34

```

```

Query Match 100.0%; Score 76; DB 1; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

```

```

RESULT 5
US-08-977-221-34
; Sequence 34, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:

```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34

Query Match 100.0%; Score 76; DB 3; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

RESULT 6
PCT-US95-06613-34
Sequence 34, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34

Query Match 100.0%; Score 76; DB 5; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

RESULT 7
US-08-346-455B-69
Sequence 69, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE


```
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-346-455B-69

Query Match 100.0%; Score 76; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFN 13
| | | | | | | | | |
Db 201 YMRPVYPTKTFN 213

RESULT 8
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69
```

Query Match 100.0%; Score 76; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 YMRPVYPTKTFN 13
| | | | | | | | | |
Db 201 YMRPVYPTKTFN 213
```

```
RESULT 9
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-69

Query Match 100.0%; Score 76; DB 5; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||

Db 201 YMRPVYPTKTFPN 213

RESULT 10
US-08-346-455B-38
Sequence 38, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613

FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 979
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-346-455B-38

Query Match 100.0%; Score 76; DB 1; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||

Db 201 YMRPVYPTKTFPN 213

RESULT 11
US-08-977-221-38
Sequence 38, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotaxin
; OTHER INFORMATION: protein sequence f
;
; US-08-977-221-38

```

```
Query Match      100.0%; Score 76; DB 3; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213

RESULT 12
PCT-US95-06613-38
; Sequence 38, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.

```

; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: putative autotaxin
; OTHER INFORMATION: protein sequence f
;
; PCT-US95-06613-38

```

```

Query Match      100.0%; Score 76; DB 5; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 YMRPVYPTKTTPN 13
| | | | | | | | | |
Db 201 YMRPVYPTKTTPN 213

RESULT 13
US-08-346-455B-67
; Sequence 67, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: N-tera 2D1 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-346-455B-67

Query Match 93.4%; Score 71; DB 1; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

RESULT 14
US-08-977-221-67
; Sequence 67, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK

; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: N-tera 2D1 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-977-221-67

Query Match 93.4%; Score 71; DB 3; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

RESULT 15
PCT-US95-06613-67
; Sequence 67, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-67

Query Match 93.4%; Score 71; DB 5; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
:|||||
Db 201 HMRPVYPTKTFPN 213

Search completed: July 19, 2001, 14:45:27
Job time: 180 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:22 ; Search time 25.97 Seconds
(without alignments)
2683.855 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSQIISLFTFAV.....RSYPEILTLKTYLHTYESEI 915
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1 A55144	autotaxin precursor
2	4306	85.8	885	1 A55453	plasma cell membra
3	2084	41.5	875	1 A57080	cell surface antig
4	1955.5	39.0	925	1 A39216	plasma cell membra
5	1899.5	37.8	905	1 A27410	plasma cell membra
6	646.5	12.9	457	2 T09932	nucleotide pyropho
7	612	12.2	496	2 T09931	nucleotide pyropho
8	611.5	12.2	479	2 T03293	nucleotide pyropho
9	610	12.2	829	2 T19494	hypothetical prote
10	609	12.1	461	2 T09933	nucleotide pyropho
11	539.5	10.7	485	2 T40657	probable phophodie
12	522	10.4	429	2 T33724	hypothetical prote
13	461	9.2	433	2 B82537	phosphodiesterase-
14	456.5	9.1	674	2 T19495	hypothetical prote
15	456	9.1	300	2 A41179	protein kinase PC-
16	410	8.2	743	2 S19437	hypothetical prote
17	335.5	6.7	493	2 S50443	hypothetical prote
18	297.5	5.9	614	2 T30973	hypothetical prote
19	241.5	4.8	133	2 T09934	hypothetical prote
20	238	4.7	96	2 A25274	phosphodiesterase
21	238	4.7	453	2 T16795	hypothetical prote
22	163	3.2	360	2 T20867	hypothetical prote
23	146.5	2.9	329	1 NCBYN1	nuclease NUC1 (EC
24	145.5	2.9	465	2 T34936	hypothetical prote
25	142	2.8	1186	2 T03180	tyrosine protein k
26	132	2.6	462	2 T36185	hypothetical prote
27	127	2.5	1820	2 A55494	latent transformin
28	123.5	2.5	454	2 A46498	glucocorticoid-sen
29	122	2.4	1374	2 S70712	protein-tyrosine k

30 121.5 2.4 2471 2 T03820 probable histidine
31 121 2.4 1888 2 T39009 hypothetical prote
32 119.5 2.4 475 2 A38340 66K glycoprotein p
33 119 2.4 2019 1 JQ1322 tenascin precursor
34 117 2.3 335 2 T11588 nuclease NUC1 (EC
35 116.5 2.3 989 2 S69711 hypothetical prote
36 112 2.2 1035 2 S61342 sulfite reductase
37 112 2.2 1394 2 A35626 transforming growt
38 112 2.2 2911 2 T20566 hypothetical prote
39 111 2.2 1394 2 A29637 position-specific
40 111 2.2 3002 2 A47221 fibrillin 1 precur
41 110.5 2.2 2871 2 A55567 fibrillin I - bovi
42 110.5 2.2 3147 2 T18674 hypothetical prote
43 110 2.2 753 2 T28787 hypothetical prote
44 109.5 2.2 476 1 SGMSV vitronectin precur
45 109.5 2.2 1472 2 S67195 probable membrane

ALIGNMENTS

RESULT 1
A55144
autotaxin precursor - human
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55144; A42329
R:Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A:Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A:Reference number: A55144; MUID:95074054
A:Accession: A55144
A:Molecule type: mRNA
A:Residues: 1-915 <MUR>
A:Cross-references: GB:L35594; NID:G537905; PIDN:AAA64785.1; PID:G537906
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A:Title: Identification, purification, and partial sequence analysis of autotaxin, a
A:Reference number: A42329; MUID:92129337
A:Accession: A42329
A:Molecule type: protein
A:Residues: 256-266;422-444;504-507,'AN';510,'X',511-515;533-548,'S',554-559,'N',561-
A:Experimental source: A2058 melanoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A:Note: a peptide fragment Tyr-Asp-Val-Pro-Trip-Asn-Glu-Thr-Ile was also found
C:Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C:Genetics:
A:Gene: GDB:ATX
A:Cross-references: GDB:378346
A:Map position: 8q22-8qter
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F:55-98/Domain: somatomedin B homology <SBH1>
F:99-142/Domain: somatomedin B homology <SBH2>
F:54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSSFQSQIISLFTFAVGVSICLGFTHRIKRAEGWEEGPPTVLSDSPWTNIGSCK 60
|||||
Db 1 MARRSSFQSQIISLFTFAVGVSICLGFTHRIKRAEGWEEGPPTVLSDSPWTNIGSCK 60

QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCKLTARGWECKDKRCGEVRNEENACHC 120
|||||
Db 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCKLTARGWECKDKRCGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVVKGESHWVDDCEEIKAECPAGFVRPPLIIFSVDFRASYMK 180

||||| 121 SEDCLARGDCTNYQVVCKGESHWDDCEEIKAACPAGFVRPPLIIFSVDGFRASYMK 180
QY 181 KGSKVMPIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWVWIPHERRILTLRLWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWVWIPHERRILTLRLWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPKKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVPAPKKRRR 360
QY 361 KIHRMDHYAAETRDQKMTNPLREIDKIVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
Db 361 KIHRMDHYAAETRDQKMTNPLREIDKIVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
QY 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIANLTCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIANLTCKKPDQHFKPYLKQH 480
QY 481 LPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
QY 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
QY 601 TRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLYRT 660
Db 601 TRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLYRT 660
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPSQNCL 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPSQNCL 720
QY 721 AYKNDKQMSYGFPPYLSSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVLVKYASER 780
Db 721 AYKNDKQMSYGFPPYLSSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVLVKYASER 780
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFILPHRDNESCSNSEDKWKVEELMKHTARVDRDIEHLTSLDFFRKTSRSYPE 900
Db 841 LSVSSFILPHRDNESCSNSEDKWKVEELMKHTARVDRDIEHLTSLDFFRKTSRSYPE 900
QY 901 ILTLKTYLHTYSEI 915
Db 901 ILTLKTYLHTYSEI 915
RESULT 2
A55453
plasma cell membrane glycoprotein PC-1, brain specific - rat
N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A55453; JU0187
R:Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
J. Biol. Chem. 269, 28235-28242, 1994
A:Title: Molecular cloning, expression, and localization of a brain-specific phosphodies
A:Reference number: A55453; MUID:95050605
A:Accession: A55453
A:Molecule type: mRNA
A:Residues: 1-885 <NAR>
A:Cross-references: GB:D28560; NID:g464196; PIDN:BAA05910.1; PID:g464197
R:Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994

A;Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase
A;Reference number: JU0187
A;Accession: JU0187
A;Molecule type: mRNA
A;Residues: 1-66,'Q',68-81,'T',83-94,'C',96,'A',98-195,'A',197-514,'E',516-621,'E',62
A;Experimental source: strain Sprague-Dawley
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester
F;54-97/Domain: somatomedin B homology <SBH1>
F;98-141/Domain: somatomedin B homology <SBH2>
F;53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status pred
F;207/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 85.8%; Score 4306; DB 1; Length 885;
Best Local Similarity 83.6%; Pred. No. 1.7e-287;
Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

QY 1 MARRSFQSCQIISLFTFAVGVSICLGTAAHRIKRAEGWEEGPPTVLSDSPWTNISGSK 60
Db 1 MARQCLGSFQVISLFTFAISVNICLGTASRIKRAE-WDEGPPTVLSDSPWTNTSGSK 59
QY 61 GRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTDRGCEVRNEENACHC 120
Db 60 GRCFELQEVGPPDCRCDNLCKSYSCCHDFDELCLKTVRGWECTDRSGEVRNEENACHC 119
QY 121 SEDCLARGDCTNYQVVCKGESHWVDD-----DCEIKAACPAGFVRPPLIIFSVDG 173
Db 120 PEDCLSRGDCCTNYQVVCKGESHWVDDAARNQSSECLQV---CP-----PPLIIFSVDG 170
QY 174 FRASYMKKSGKVMPIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSM 233
Db 171 FRASYMKKSGKVMPIEKLKSCGTHVPYTRPVYPTKTFPNLYTLATGLYPESHGIVGNSM 230
QY 234 YDPVFDATEFHLRGREKFNHRWGGQPLWITATKQGVKAGTFWVWIPHERRILTLRLWL 293
Db 231 YDPVFDATEFHLRGREKFNHRWGGQPLWITATKQGVAGTFWVWVSIPIHERRILTLQWL 290
QY 294 TLPDHERPSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRRQERPVA 353
Db 291 SLPDNERPSVYAFYSEQPDFSGHKYGFPGPE----- 321
QY 354 PPKRRRKIHRMDHYAAETRDQKMTNPLREIDKIVGQMDGLKQLKLRRCVNVIFVDHG 413
Db 322 -----MTNPLREIDKTVGQMDGLKQLRLHRCVNVIFVDHG 358
QY 414 MEDVTCDRTEFLSNLYTNVDDITLVPGTGLGRIRSKFSNNAKYDPKAIANLTCKKPDQHF 473
Db 359 MEDVTCDRTEFLSNLYTNVDDITLVPGTGLGRIRAKSINNSKYDPKTIANLTCKKPDQHF 418
QY 474 KPYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKKPSGKCFQGDHGFNDKV 533
Db 419 KPYMKQHLPKRLHYANNRRIEDIHLVDRRWHVARKPLDVYKKPSGKCFQGDHGFNDKV 478
QY 534 NSMQTVFVGYGPTFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFR 593
Db 479 NSMQTVFVGYGPTFKYRTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRLTNTFR 538
QY 594 PTMPEVTRPNYPGIMYLOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGTE----- 645
Db 539 PTMPDEVSRPNYPGIMYLOSEFDLGCTCDDKVEPKNKLEELNKLRLHTKSGTEAETGKFRG 598
QY 646 -----ERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTV 688
Db 599 SKHENKKNLNGSVEPRKERHLLYGRPAVLYRTSYDILYHTDFESGYSEIFLMLLWTSYTI 658
QY 689 SKQAEVSSVPDHLTSCVRPDVVRVSPSQNCLAYKNDKQMSYGFLLPPLSSSPEAKYDA 748
Db 659 SKQAEVSSIPHELTNCVRPDVVRVSPGFSQNCCLAYKNDKQMSYGFLLPPLSSSPEAKYDA 718
QY 749 FLVTNMVPMYPAKRVWNYFORVLVKYASERNGVNISGPIFDYDGLHDTEDKIKQY 808
Db 719 FLVTNMVPMYPAKRVWAYFORVLVKYASERNGVNISGPIFDYDGLRDTEDIKQY 778

QY 809 VEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCSSEDESKWV 868
Db 779 VEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCSSEDESKWV 838

QY 869 EELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 915
Db 839 EELMKMHTARVRDIEHLTGLDFYRKTSRSYSEILTLKTYLHTYSEI 885

RESULT 3
A57080
cell surface antigen RB13-6 - rat
N;Contains: phosphodiesterase I (EC 3.1.4.1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A57080
R;Deissler, H.; Lottspeich, F.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A;Title: Affinity purification and cDNA cloning of rat neural differentiation and tumor
A;Reference number: A57080; MUID:95247775
A;Accession: A57080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-875 <DEI>
A;Cross-references: GB:247987; NID:g806378; PIDN:CAA88029.1; PID:g806379
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; su
F;1-22/Domain: cytosolic #status predicted <CYT>
F;23-45/Domain: transmembrane #status predicted <TMM>
F;46-875/Domain: extracellular #status predicted <EXT>
F;51-94/Domain: somatomedin B homology <SBH>
F;95-138/Domain: somatomedin B homology <SBH2>
F;206/Binding site: AMP (Thr) (covalent) #status predicted
F;237,280,289,533,574,702,789/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 41.5%; Score 2084; DB 1; Length 875;
Best Local Similarity 43.5%; Pred. No. 5e-135;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

QY 57 GSKGRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116
Db 53 GSKRKKCFDSSHRGLEGRCDGCTDRGDCWDFEDTCVKSTQIWTCSFRCGETRLEAA 112

QY 117 ACHGSEDCIARGDCCTNYQVCKGESHVWDDCEIEKAAECFAGFVRPLIIFSVDFGRA 176
Db 113 LCSCADDCLQRKDCCTDYKAVCQGEVFWVTEACASSQEPQCEGDFQDPVILFSDMGFRA 172

QY 177 SYMKKGSKVPNIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP 236
Db 173 EYLQTWSTLLPNINKLTKTGLHSHKYMAMYPKTFPNHYTIVTGLYPESHGIIDNNMYDV 232

QY 237 VFDATFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SV 278
Db 233 YLNKNFSLSSVEKSNPAWWSGQPLWLTAMYQGLKAASYWLGSDVAVNGSFPNIYRNSN 292

QY 279 VIPHERILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGFPGPERSYGSFPETPAKRP 338
Db 293 SVPYESRIATLLQWLDLPKAERPSFYTIYVEEPDSAGHSGPV-----SAG----- 338

QY 339 KRKVAPKRRQERPVPAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKIVGQIMDLGKLQ 398
Db 339 -----VIKALQLVDDAFGLMEGLKQR 360

QY 399 KLRRCVNIVFGDHGMEDVTCDRTEFLSNLYTNVDDITLVPGLGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDDQTSQDRVEYMTDYFPEI-NFYMYQGPAPRIETRNIPQDFFTFN 419

QY 453 AKYDPKAIIANLTCKKPDQHKPYLKQHLPKRLHYANNRRRIEDIHLVERRRHHVARKPLD 512
Db 420 S----EEIVRDLSCRKSDQHKFKPYLTPDLPKRLHYAKNVRIDKVLHLMVDQWLAYR---- 471

QY 513 VYKPSGKCFQDGHGFDNKVNSMQTVFVGYPGTFKYKTKVPPFENIELYNVCMCDLLGLK 572
Db 472 --NKGSSNC-EGTHGYNNEFKSMEAIFLAHGPSFKETKTVIEFENIEVYNLLCDLLHIQ 528

QY 573 PAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQPSHAEELSKSACGFTTTPLPKDSLNCSC-LALQTSQEE 587

QY 633 ELNKRLLHTKG----STEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687
Db 588 QVNQRLNLSGGEVSATEKTNLDFGRPRVIOQNKDCHLLYHREYVSGFGKAMKMPWSSYT 647

QY 688 VSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCLAYKNDKQMSYGFLEPPYLSSSPEAKYD 747
Db 648 VPKPGDTSSLPTPTVPCDLRADVRVDPSESQKCSFYLADQNIDHGFLYPPAIGNNESQYD 707

QY 748 AFLVTNMVPMYPAFKRVVNYFORVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIKQ 807
Db 708 ALITSNLVPMYKEFKKMDYFHKVLLIKYAIERNGVNVSGPIFDYNDYDGHFDAPDEITN 767

QY 808 YVEGSSIPVTHYYSIIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCSSEDESKW 867
Db 768 YVAGTDVPVPTHYFVVLTSCKNKTHTPDSCPGWLDVLPFVVPVHRPTNVESCPENKAEDLW 827

QY 868 VEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYSEI 915
Db 828 VEERFKAHARVRDVELLTGLDFYQEKTPQVSEILQLKTYLPTFTETII 875

RESULT 4
A39216
plasma cell membrane glycoprotein PC-1 - human
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A39216; S21706; S23587; S51030
R;Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A;Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
A;Reference number: A39216; MUID:91009202
A;Accession: A39216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-925 <BUC>
A;Cross-references: GB:J05654
R;Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A;Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
A;Reference number: S21706; MUID:92246539
A;Accession: S21706
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-925 <FUN1>
A;Accession: S23587
A;Molecule type: protein
A;Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364;449-465;4
A;Note: it is uncertain whether Met-1 or Met-53 is the initiator
R;Belli, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A;Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph
A;Reference number: S51030; MUID:95094801
A;Accession: S51030
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-80 <BEL>
C;Genetics:
A;Gene: GDB:PDNP1; M6S1; NPPS
A;Cross-references: GDB:132615; OMIM:173335
A;Map position: 6q22-6q23
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; t
F;77-97/Domain: transmembrane #status predicted <TMM>

F:104-144/Domain: somatomedin B homology <SBH1>
F:145-188/Domain: somatomedin B homology <SBH2>
F:179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) #s
F:256/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 39.0%; Score 1955.5; DB 1; Length 925;
Best Local Similarity 42.2%; Pred. No. 3.5e-126;
Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19;

QY 58 SCKGRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENA 117
| | | | | : | : | | | : | : | | | : | : | | | : | : | | | :
Db 107 SCKGRCFE-RTFG--NCRCDAAACVELGNCCLDYQETCIEPEHIWTCNKFRCGEKRLTRSL 163
QY 118 CHCSEDCIARGDCCTNYQVCKGESHVDDDCETKAAECAGFVRPPLIIFSVDGFRAS 177
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 164 CACSDCKDKGDCINYSVVCQGEKSWVEEPCESINEPQCPAGFETPTLLFSLDGFRAE 223
QY 178 YMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 224 YLHTWGGLLPVISKLKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGIIDNKMYDPK 283
QY 238 FDATEFHLRGREKFNHRWGGQPLWITATKQGVKAGTFW-----SVV 279
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 284 MNASFSLKSKEKFNPEWKGEPIWVTAKYQGLKSGTFFWPGSDVEINGIFPDIIKMYNGS 343
QY 280 IPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPFPAKRPK 339
: | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db 344 VPFEERILAVLQWLQPKDERPHFYTTYLLEEPSDSSHSGYGPVSSE----- 388
QY 340 RKVAPKRRQERPVPAPPKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQMLDGLKOLK 399
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 389 -----VIKALQRVDGMVGMMLDGLKELN 411
QY 400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGLTGRIR-----SKFSNNAK 454
| | | | | : | | | | | : | : | : | : | : | : | : | : | : | :
Db 412 LHRCLNLILISDHGMEOGSCCKYIYLNKYLGDVKNKVIYGPAARLRPSDVPDKYIS--- 468
QY 455 YDPKAIIANLTCKPDQHFKPYLKQHLPKRLHYANNRIEDIHLLVERRWHVARKPLDVI 514
: : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 469 FNYEGIARNLSCREPNQHFKPYLKHFLPKRLHFAKSDRIEPLTFYLDPOWQALNPSE-- 526
QY 515 KPSPGKCFQGDHGFNDKVNNSMQTVFVGYPGTFYKTKVPPFENIELYNVMDLLGLKPA 574
: | | | | : | | | | : | : | : | : | : | : | : | : | : | : |
Db 527 RKYCG----SGFHGSDNVFSNMQALFVGYPGFGKHGIEADTFENIEVYNLMCDLLNLTPA 582
QY 575 PNNGTHGSLNHLRTNFRPTMPEEVRPNYPGIMYLQSDF-----DLGCTCDDKVEPK 628
| | | | | : | | | | | : | : | : | : | : | : | : | : | : | :
Db 583 PNNGTHGSLNHLKNPVYTPKHPKEV---HP---LVQCPFTRPNRDLGSCNPSILP- 634
QY 629 NKLDELNKLRLHTKGSTEE--RH--LLYGRPAVLYR-TRYDILYHTDFESGYSEIFLMLW 683
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 635 --IEDFQTQFNLTVAEKKIHKETLPYGRPRVLQKENTICLLSQHFMSGYSQDILMPLW 692
QY 684 TSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCILAYKNDKQMSYGFLEPPYLSSSPE 743
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 693 TSYTVDRNDSFST--EDFSNCLYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPPLKNSS 750
QY 744 AKY-DAFLVTNMVMPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDYGDLHDE 802
| : | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 751 GIYSEALLTNIIVMQSFQVIWRYFHDTLRLKYABERNGVNVSGPVDFDYDGRCDL 810
QY 803 DKIKQ---YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESC 859
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 811 ENLRQKRRVIRNQEILIPHTFFIVLTSCKDTSQTPLHCEN-LDTLAFILPHRTDNSESCV 869
QY 860 SSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRKSYPEILTLKTYLHTYESE 914
: : | | | : | | | : | : | : | : | : | : | : | : | : | : | :
Db 870 HGKHDSSWVEELMLHARITDVEHITGLSFYQQRKEPVSDILKLTPLTFESQE 924

RESULT 5
A27410

plasma cell membrane glycoprotein PC-1 - mouse
N;Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A27410; I59055; S38354
R;van Driel, I.R.; Goding, J.W.
J. Biol. Chem. 262, 4882-4887, 1987
A;Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA
A;Reference number: A27410; MUID:87165906
A;Accession: A27410
A;Molecule type: mRNA
A;Residues: 1-905 <VAN>
A;Cross-references: GB:J02700; NID:g200236; PIDN:AAA39893.1; PID:g200237
A;Note: the authors translated the codon CAG for residue 24 as Glu
R;van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985
A;Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and anal
A;Reference number: I59055; MUID:86094275
A;Accession: I59055
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 203-219 <RES>
A;Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235
R;Belli, S.I.; van Driel, I.R.; Goding, J.W.
Eur. J. Biochem. 217, 421-428, 1993
A;Title: Identification and characterization of a soluble form of the plasma cell mem
A;Reference number: S38354; MUID:94039066
A;Accession: S38354
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 35-219 <BEL>
A;Cross-references: EMBL:L04516
C;Genetics:
A;Introns: 62/3; 87/1; 126/1; 168/1; 188/2
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; t
F;86-126/Domain: somatomedin B homology <SBH1>
F;127-170/Domain: somatomedin B homology <SBH2>
F;161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predict
F;238/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 37.8%; Score 1899.5; DB 1; Length 905;
Best Local Similarity 41.0%; Pred. No. 2.4e-122;
Matches 365; Conservative 155; Mismatches 262; Indels 109; Gaps 16;
QY 58 SCKGRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENA 117
| | | | | : | | | | | : | : | | | : | : | | | : | : | | | :
Db 89 SCKGRCFERTFS--NCRCDAAACVSLGCCLDLDFQETCVEPTHIWTCNKFRCGEKRLSRFV 145
QY 118 CHCSEDCIARGDCCTNYQVCKGESHVDDDCETKAAECAGFVRPPLIIFSVDGFRAS 177
| | | | | : | | | | | : | : | | | : | : | | | : | : | | | :
Db 146 CSCADDCKTHNDCCINYSVVCQDKKSWVEETCESIDTPECPAEFESPTLLFSLDGFRAE 205
QY 178 YMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 206 YLHTWGGLLPVISKLKNCGYTKNMRPMYPTKTFPNHYSIVTGLYPESHGIIDNKMYDPK 265
QY 238 FDATEFHLRGREKFNHRWGGQPLWITATKQGVKAGTFW-----SVV 279
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 266 MNASFSLKSKEKFNPLWYKGQPIWVTANHQEVKSGTYFWPGSDVEIDGILPDIIKMYNGS 325
QY 280 IPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPFPAKRPK 339
: | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db 326 VPFEERILAVLEWLQPSHERPHFYTTYLLEEPSDSSHSGHPVSSE----- 370
QY 340 RKVAPKRRQERPVPAPPKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQMLDGLKOLK 399
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 371 -----VIKALQKVDRLVGMMLDGLKDLG 393
QY 400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGLTGRIPSKFSNNAKY--DP 457
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 394 LDKCLNLILISDHGMEQGSCKKYVYLNKYLGDVNNKVYGPAAARLPTDVPETYYSFNY 453

QY	452	NAKYDPKAIILANTCKKPDQHFKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPL	511
Db	142	IAKSD-----RIERLTFYLDPQWQALNPS	166
QY	512	DVYKKPSGKCFFQGHDGNKVNSMQTVFVGCGPTFKYKTVPFFENIELYNVMCDLGL	571
Db	167	E--RKYCG--GGFHGSDNLFLNMQALEFXXXXXXXHSTEVDSFENIEVYNLMCDLLNL	220
QY	572	KPAPNNGTHGSLNHLLRTNTFRPTMPEEVRPNYPGIMYLQSDFDLGCTCDDKVEPKNKL	631
Db	221	TPAPNNGTH-----	229
QY	632	DELNKRHLTKGSTEEERHLLYGRPAVLRYTRYDILYHTDFESGYSEIFMLLLWTSYTVSKQ	691
Db	230	-----	229
QY	692	AEVSSVPDHLTSCVRPDVRSVSPFSQNCLAYKNDKQMSYGFLFPPLYSSSPEAKY-DAFL	750
Db	230	-----LSYGFLSPPOLHKHGSSQVYSEALL	253
QY	751	VTNMPMPYPAFKRVWNFYQRLVLVKKYASERNGVNVISGPIDYDYDGLHDTEDIKQYVE	810
Db	254	TINIVPMYQSFOVI-----	267
QY	811	GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSESDESKWVEE	870
Db	268	-----HESLWVEE	275
QY	871	LKMKHITARVRDIEHLTSLDFFRK	893
Db	276	-----	298

Search completed: July 19, 2001, 14:45:54
Job time: 152 sec

QY	107	RCGEVRNEENACHCSEDC	LARGDCC	TNYQVVCKGESHWVDD	DCEEIKAAEC	PAGFVRPPL	166
		:	:	: : :			
Db	2	RCFE-RTFGN-CRCDAA	CVELGNCCLD-				26
QY	167	IIFSVDGFRA	SYMKGSKVM	PNIEKLRSCTHSPYMRPVYPTKTFFPNLYLATGLYPESH			226
Db	27			NMRPVYPTKTFPNHYHSIVTGLYPESH			52
QY	227	GIVGNSMYDPVEDATFH	LRGREKNHRWWGGQPLWITATKQGVKAGTEFW-				276
		:	: :	: :	: :		
Db	53	GIIDNK-		-GEPILWTA-	--KSGTFWP	GS	83
QY	277	-----SVVIPHERRI	LTLRLTPDH	RPSVYAFYSEQPDFSGHKYGCPGP	EESY	GSP	331
		:					
Db	84	FPDYXVSVPFEERILA	ILKWQLP-				108
QY	332	FTPAPRRPKRVAPKRRO	ERPAPPKKRRRKIHRMDHYAAET	RQDKMTNP	LEIDKIV	QOL	391
Db	109	-----					108
QY	392	MDGLKQLKLRRCVNVI	FVGDHGMEDVTCDRT	EFLSNYLTNVDDITLVP	GT	LGIRSKFSN	451
		: : : :	:				
Db	109	---KELNLH	RCLNLILISDHGME	QSCKYYSF-			141

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:44:18 ; Search time 16.91 Seconds
(without alignments)
1853.564 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSQIISLFFAV.....RSYPEILTLKTLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1955.5	39.0	873	1	PC1_HUMAN
2	1899.5	37.8	871	1	PC1_MOUSE
3	410	8.2	743	1	YCR6_YEAST
4	335.5	6.7	493	1	YEB6_YEAST
5	238	4.7	61	1	PPD1_BOVIN
6	146.5	2.9	329	1	NUC1_YEAST
7	123	2.5	4655	1	LRP2_HUMAN
8	122	2.4	1323	1	LT23_CAEEL
9	121	2.4	1888	1	YDT2_SCHPO
10	119.5	2.4	252	1	NUC1_CUNEE
11	119.5	2.4	475	1	VTNC_RABIT
12	117	2.3	335	1	NUC1_SCHPO
13	116.5	2.3	989	1	YD30_YEAST
14	112	2.2	1394	1	TGFB_HUMAN
15	111.5	2.2	299	1	NUCG_BOVIN
16	111	2.2	1396	1	ITAZ_DROME
17	111	2.2	2871	1	FBN1_HUMAN
18	110.5	2.2	294	1	NUCG_MOUSE
19	110.5	2.2	478	1	VTNC_MOUSE
20	110.5	2.2	2871	1	FBN1_BOVIN
21	110	2.2	753	1	YJ05_CAEEL
22	109.5	2.2	1472	1	ATC9_YEAST
23	108.5	2.2	320	1	NUC1_SYNRA
24	108	2.2	1065	1	YD22_SCHPO
25	106	2.1	1106	1	STC_DROME
26	106	2.1	1178	1	YNI7_YEAST
27	106	2.1	2204	1	RRPL_NDVB
28	106	2.1	2871	1	FBN1_MOUSE
29	106	2.1	3099	1	POLG_PEMVM
30	105.5	2.1	1612	1	MTDM_PARLI
31	105.5	2.1	1808	1	TENA_CHICK
32	104.5	2.1	2201	1	TENA_HUMAN
33	104.5	2.1	4289	1	TENX_HUMAN

34	104	2.1	470	1	BFR1_YEAST	P38934	saccharomyc
35	104	2.1	659	1	AMIA_STRPN	P18791	strepococc
36	104	2.1	700	1	KPC2_DROME	P13677	drosophila
37	104	2.1	969	1	DPOM_NEUIN	P33538	neurospora
38	103.5	2.1	297	1	NUCG_HUMAN	Q14249	homo sapien
39	103	2.1	755	1	P100_HSV7J	P52519	human herpe
40	103	2.1	1700	1	BAR3_CHITE	Q03376	chironomus
41	102.5	2.0	369	1	PP11_HUMAN	P21128	homo sapien
42	102.5	2.0	747	1	FHUA_ECOLI	P06971	escherichia
43	102.5	2.0	1426	1	EGFR_DROME	P04412	drosophila
44	102	2.0	563	1	IDS_MOUSE	Q08890	mus musculu
45	102	2.0	1018	1	FNBA_STAAU	P14738	staphylococ

ALIGNMENTS

RESULT 1
PC1_HUMAN
ID PC1_HUMAN STANDARD; PRT; 873 AA.
AC P22413; Q9Y6K3; Q9UP61;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
DE (EC 3.6.1.9) (NPPASE)].
GN PDNP1 OR PC1 OR NPPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91009202; PubMed=2211644;
RA Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.;
RT "Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
RT molecule, amino acid sequence, and chromosomal location.";
RL J. Biol. Chem. 265:17506-17511(1990).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=92246539; PubMed=1315502;
RA Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
RA Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
RA Yamashina I.;
RT "Molecular cloning of cDNAs for human fibroblast nucleotide
RT pyrophosphatase.";
RL Arch. Biochem. Biophys. 295:180-187(1992).
RN [3]
SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
RX MEDLINE=99408501; PubMed=10480624;
RA Pizzutti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
RA Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
RA Tassi V., Trischitta V.;
RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
RT region is strongly associated with insulin resistance.";
RL Diabetes 48:1881-1884(1999).
CC -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
CC -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
CC OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
CC OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
CC -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623(1985).
-!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
OLIGO-NUCLEOTIDES.
-!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF
ANTIBODY-SECRETING CELLS.
-!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: J02700; AAA39893.1; ALT_INIT.
EMBL: M12552; AAA39892.1; -.
PIR: A27410; A27410.
MGD: MGI:97370; Pdnpl.
InterPro: IPR001212; -.
InterPro: IPR002591; -.
Pfam: PF01663; Phosphodiester; 1.
Pfam: PF01033; Somatomedin_B; 2.
PRINTS: PR00022; SOMATOMEDIN_B.
PROSITE: PS00524; SOMATOMEDIN_B; 2.
KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase.
FT MOD_RES ?1 ?1 BLOCKED.
FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 46 871 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 871 AA; 99487 MW; 80848F81071F70AA CRC64;

Query Match 37.8%; Score 1899.5; DB 1; Length 871;
Best Local Similarity 41.0%; Pred. No. 1.7e-129;
Matches 365; Conservative 155; Mismatches 262; Indels 109; Gaps 16;

QY 58 SCKGRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENA 117
| | | | | : : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 55 SCKGRCFERTFS---NCRCDAACVSLGNCCLDFQETCVEPTHWTCTNKFRCGEKRLSRFV 111
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 118 CHCEDCLARGDCCTNYQVCKGESHVWDDCEEIKAAECPCAGFVRPPLIIFSVDFGRAS 177
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 112 CSCADDCKTHNDCCINYSVCQDKKSWVEETCESIDTPECPAEFESPTLLFSLDGFRAE 171
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 178 YMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 172 YLHTWGLLPVISKLNCGYTKNMRMPYPTKTFPNHYSIVTGLYPESHGIIDNKMYDPK 231
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 238 FDATEHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SVV 279
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 232 MNASFSLKSKEKFNPLWYKQPIWVTANHQEVKSGTYFWPGSDVEIDGILPDYKVYNGS 291
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 280 IPHERRILTLRLWLPDHERPSVYAFYSEQPDFSGHKYKPGFPESSYGSFPTPAKRPK 339
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 292 VPFEERILAVLEWLQPLSHERPHFYTLYLEEPDSSGSHGPVSSE----- 336
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 340 RLVAPKRRQERPVPAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKIVGQMLDKLQK 399
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 337 -----VTKALQKVDRLVGMMLMDGLKDLG 359
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPCTLGRIRSKFSNNAKY--DP 457
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 360 LDKCLNLILISDHGMEQGCKKYVYLNKYLGDVNVKVVYGPAAARLPTDVPETYISFNY 419
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 458 KAIIANLTCKKPDQHFYKPKLQHLPKRLHYANNRRIEDIHLVERRHWVARKPLDVYKPK 517
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 420 EALAKNLSCREPNQHFYKPKLQHLPKRLHYANNRRIEDIHLVERRHWVARKPLDVYKPK 477
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 518 SGKCFQDGHGDNKVNMQTVFVGYGPTFKYKTKVPPFFENIELYNVMDLLGLKLPAPNN 577
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 478 CG----SGFHGSDNLFNSMQALFIGYGPAPKHAEGVDSFENIEVYNMCDLLGLIPAPNN 533
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 578 GTHGSLNHLRLTNTFRPTMPEEVTNPYPGIM----YLOSDFDLCTCDDKVEPKNKLDE 633
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 534 GSHGSLNHLRLTNTFRPTMPEEVTNPYPGIM----YLOSDFDLCTCDDKVEPKNKLDE 584
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 634 LNKRLHTKSTGERHLL-----YGRPAVLRYTRY-DILYHTDFESGYSEIFLMLLWTSYT 687
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 585 FEKQLNL--TTEDDDIYHMTVPYGGPRILLKQHVCLLQOQQFLTGYSLDLLMPLWASYT 642
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 688 VSKQAEVSSVPDHLTSCVRPDRVSPFSQNCCLAYKNDKQMSYGLFPPYLSSSPEAKY- 746
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 643 FLRNDQFSR--DDFSNCMYQDLRIPLSPVHKCSYKSKLSYGLFPPYLSSSPEAKY- 700
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 747 DAFLVTNMPMPYPAKRVNRYFQRLVVKYASERNVNVISGPIFYDYDGLDHTEDKIK 806
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 701 EALLTSNIVPMYQSFQVWHYLDLTLQRYAHERNGINVVSGPVDFDYDGRYDSLEILK 760
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 807 Q---YVEGSSIPVPTHYISITSCLDFTQPADKCDGCPISVSSFILPHRPDNEESCNSSED 863
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 761 QNSRVIRSQEILIPTHFEIVLTSCQLSETPLECSA-LESSAYILPHRPDNIESTHGKR 819
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 864 ESKWVEELMKMHTARVDIEHLTSLDFRKTSTRSYPEILTKTYLHTYSE 914
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 820 ESSWVEELLTHRARVTDVELITGLSFYQDRQESVSELLRLKTHLPIFSQE 870
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 3
YCR6_YEAST STANDARD; PRT; 743 AA.
ID YCR6_YEAST
AC P25353;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 84.9 KDA PROTEIN IN PMPI-FEN2 INTERGENIC REGION.
GN YCR026C OR YCR26C OR YCR246.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-244 FROM N.A.
RA Pohl F., Richterich P., Wurst H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 244-743 FROM N.A.
RX MEDLINE=92245758; PubMed=1574926;
RA Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.;
RT "The complete sequence of K3B, a 7.9 kb fragment between PK1 and
RT CRY1 on chromosome III, reveals the presence of seven open reading
RT frames.";
RL Yeast 8:205-213(1992).
CC -!- SIMILARITY: TO YEAST YEL016C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC


```
DR EMBL; X59720; CAA42318.1; --
DR PIR; S19437; S19437.
DR PIR; S27380; S27380.
DR SGD; S0000621; YCR026C.
DR InterPro; IPR002591; -.
DR Pfam; PF01663; Phosphodiesterase 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

Query Match      8.2%; Score 410; DB 1; Length 743;
Best Local Similarity 24.0%; Pred. No. 5.4e-22;
Matches 126; Conservative 76; Mismatches 178; Indels 146; Gaps 18;

QY 164 PPLIIFSDGFRASYM-KKGSKVMPIEKLKSCG-----THSPYMRPVYPTKTFPNLYTLA 218
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 168 PLTIVISLDGFHPSLISKRTNTPFLHDLIELKYGDMNITSTPFMIPSFPTETFPNHWTLV 227

QY 219 TGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGG---QPLWITATKQ-----GVK 270
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 228 TGQYPIHHGIVSNVFWDPDLNEEFH---PGVLDPRIWNNDTEPIWQTVQSAFDGDIPIFK 284

QY 271 AGTFFW-----SVPVIPHERILTLRLWLT 294
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 285 AATHMWPGSVNYTKYTEKLQPEHKKPIARERTPFYDFEFNAKEPLSQKLSKLIIEYVD 344

QY 295 LPD-HERPSVYAFYSEQPDFSGHKYGPFGPESSYSGSPFPAKRPKRKVAPKRRQERPVA 353
      : : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 345 MSTLNERPQLILGYVPNVDAFGKHG--YPSESEY-----377

QY 354 PPKRRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHG 413
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 378 -----YY-----EDFTETLGEVDTFLKQLVESLQERNLTSFTNLVIVSDHG 418

QY 414 MEDVTCD-----RTEFLSNYLTNVDDITLVPGLTGLRIRSKFSNNAKYDPKA 459
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 419 MSDIVVPSNVIWEDLLDEKLKRDYVSH-----AYLEGPMMAISLKDSGNI-----NE 466

QY 460 IIANLTCKKPDQHKPYLKQHLPKRLHY--ANNRRIEDIHLLVERRWHVARKPL----- 511
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 467 VYHNLTSTIDEDKYTVYVNGNFKPEWNFNDGKNHHMASIWIIVPEPGYAVMKKEQLKKVAK 526

QY 512 -DVYKKPSGKCFQGDHGFNDKVNMQTVFVGYGPTFKYKTKVPPFENIELYNVMDLLG 570
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 527 GDHKDKNEDNVFTIGSHGYDNNAIDMRSVFIGMGYPFP-QGYIEPFQNTIYINLLCDICG 585

QY 571 LKPAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPGIMYLOSDFD 616
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 586 VAEKDRNSNDGT--GMLMNQLREPOQSSEVE-----IEDDFD 620

RESULT 4
YEB6_YEAST
ID YEB6_YEAST STANDARD; PRT; 493 AA.
AC P39997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
GN YEL016C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
```

```
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YCR26C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U18530; AAB64493.1; -.
DR SGD; S0000742; YEL016C.
DR InterPro; IPR002591; -.
DR Pfam; PF01663; Phosphodiesterase 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 57354 MW; 10E67A05C6DEDF09 CRC64;

Query Match      6.7%; Score 335.5; DB 1; Length 493;
Best Local Similarity 24.8%; Pred. No. 7.6e-17;
Matches 116; Conservative 71; Mismatches 153; Indels 127; Gaps 21;

QY 167 IIFSVDGFRASYM-KKGSKVMPIEKLKSCG---THSPYMRPVYPTKTFPNLYTLATGL 221
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 79 ILISIDGFHPLIDAKYTPFLYNLHNLRSYDMMNITAPYMIPSFPTQTFPNHWSMTGK 138

QY 222 YPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGG--GQPLW--ITATKQG-VKAGTFFW 276
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 139 YPIEHGIVSNIFWDFNFTSSEFR--PNNLDARIWSNTADPIWQLQLQTESQGEYKVATHMW 195

QY 277 ---SVV-----IPHER-----RILTILRLTLPD-HERPSVYAFYSEQ 310
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 196 PGSEVVYEDHGDVPRERMPFYFGKFNQWEKLDKLAIFYRIDMPQLKDRPELVISYIPN 255

QY 311 PDFSGHKYGPFGPESSYSGSPFPAKRPKRKVAPKRRQERPVPAPPKRRRKIHRMDHYAA 370
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 256 VDSYGHSGF-----Y 265

QY 371 ETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEF----- 424
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 266 DLDRKRLQKLIGEVDGFFLDLIEGLQKRLKISNVMIVSDHGMNSVNANDGEHVWVWER 325

QY 425 -----LSNYLTNVDDITLVPGLTGLRIRSKFSNNAKYDPKAIIANLTCKKPDQ---HFKP 475
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 326 VFPADAMSAFISHLYN---EGPMMVCLKNPRDKQWICDLIEAQLEKAYGDEISRKFHV 381

QY 476 YLKQHLN---KRLHYANNR-----RIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDH 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 382 ILKEDFDPKWKYFYDNRKHYRDDRGDIWLADYYAIVKEMGDV---PIG---IMGTH 435

QY 528 GFD-NKVNMQTVFVGYGPTFKYKTKVPPFENIELYNVMCD---LLG 570
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 436 GYNFNCSDMASIFIGMGPMFNEV-VPPFENIEVYNMLIKASALLG 481

RESULT 5
PPD1_BOVIN
ID PPD1_BOVIN STANDARD; PRT; 61 AA.
AC P15396;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE
DE PHOSPHODIESTERASE) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
```


SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=85234541; PubMed=2989287;
RA Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;
RT "Amino acid sequence of the active site peptide of bovine intestinal
RT 5'-nucleotide phosphodiesterase and identification of the active
RT site residue as threonine.";
RL J. Biol. Chem. 260:8320-8324(1985).
CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
DR PIR; A25274; A25274.
KW Hydrolase.
FT NON_TER 1 39
FT ACT_SITE 39
SQ SEQUENCE 61 AA; 6999 MW; 580C8B4807A61C84 CRC64;

Query Match 4.7%; Score 238; DB 1; Length 61;
Best Local Similarity 66.7%; Pred. No. 5.4e-11;
Matches 40; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 172 DGFRA5YMKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGN 231
Db 1 DGFRAEVLQWSTLVPNINKLTCGVHSQYLRLPAYPTKTFPNHYTIVTGLYPESHGIIDN 60

RESULT 6
NUCL_YEAST
ID NUCL_YEAST STANDARD; PRT; 329 AA.
AC P08466;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
GN NUC1 OR YJL208C OR J0310 OR HRE329.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2935-106;
RX MEDLINE=88233924; PubMed=2836792;
RA Vincent R.D., Hofmann T.J., Zassenhaus H.P.;
RT "Sequence and expression of NUC1, the gene encoding the mitochondrial
RT nuclease in Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 16:3297-3312(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95274326; PubMed=7754713;
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
RT X identifies 24 open reading frames including NUC1, PRP21 (SPP91),
RT CDC6, CRP2, the gene for S24, a homologue to the aconitase gene ACO1
RT and two homologues to chromosome III genes.";
RL Yeast 10:1235-1249(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95242842; PubMed=7725802;
RA Vandenbol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
RA Hilger F.;
RT "Sequence analysis of a 40.2 kb DNA fragment located near the left
RT telomere of yeast chromosome X.";
RL Yeast 10:1657-1662(1994).
RN [4]
RP SEQUENCE OF 204-329 FROM N.A.
RX MEDLINE=90014786; PubMed=2552292;
RA Liu Y., Dieckmann C.L.;
RT "Overproduction of yeast viruslike particles by strains deficient in
RT a mitochondrial nuclease."

RL Mol. Cell. Biol. 9:3323-3331(1989).
CC -1- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
CC -1- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06670; CAA29870.1; -
DR EMBL; X77688; CAA54748.1; -
DR EMBL; Z34098; CAA84003.1; -
DR EMBL; Z49483; CAA89505.1; -
DR EMBL; M28067; AAA34457.1; -
DR PIR; S05888; NCBYN1.
DR PIR; S46621; S46621.
DR HSSP; P13717; 1SMN.
DR SGD; S0003744; NUC1.
DR InterPro; IPR001604; -
DR Pfam; PF01223; Endonuclease; 1.
DR PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
KW Hydrolase; Nuclease; Endonuclease; Magnesium; Mitochondrion;
KW Inner membrane.
FT ACT_SITE 138 BY SIMILARITY.
SQ SEQUENCE 329 AA; 37209 MW; CAEC9678CB00943C CRC64;

Query Match 2.9%; Score 146.5; DB 1; Length 329;
Best Local Similarity 22.8%; Pred. No. 0.002;
Matches 79; Conservative 48; Mismatches 159; Indels 61; Gaps 16;

QY 565 MCDLLGLKPPANNNGTHGSLNHLRLTNTFRPTMPEVTRPNYPGIMYLSQDFDLGCTCDDK 624
Db 1 MCSRLLSGLVGLGAGTGLTYLL-LNKHSTP---QIIETPYP----- 38

QY 625 VEPKNKLDLNLKRLHTKSGTEERHLLYGRPAVLRYTRYDILYHTDFESGYSEIFLMLWT 684
Db 39 --PTQKPNS-NIQSHSFNVDPSPGFFKYGPGPI----HDLQNRREEFISYCNRQTQNPYVW 91

QY 685 SYTVSKQAEVSSVPDHLTSCVRPDVRSVSPFSQNCLAYKNDKQMSYGLFPPY-LSSSPE 743
Db 92 LEHITPESLAARNADRKNSEFFKEDEVIPEKFRGKLRDYFR-SGYDRGHQAPAAAKFSQQ 150

QY 744 AKYDAFLVTNMVPMY-PAFKR-VW---NYFQRLVVKKVASERNGVNVISGPIFDYDGL 798
Db 151 AMDDTFYLSNMCPOVGEFNRDYNWAHLEYFCRGLTKKYKS----VRIVTGPLYLPKKDPI 206

QY 799 HDTEDKIKQYVEGS--SIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRP-DNE 855
Db 207 -DNKFRVNYEVIGNPPSIAVPTHTFFKLIVAEAPTANPARE---DIAVAAFVLPNEPISNE 262

QY 856 ESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFKTSRSYPEIL 902
Db 263 TKLTDFE-----VPIDALERSTGLELLQKVPSPSKKAL 295

RESULT 7
LRP2_HUMAN
ID LRP2_HUMAN STANDARD; PRT; 4655 AA.
AC P98164; O00711; Q16215;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
DE (GLYCOPROTEIN 330).
GN LRP2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96305376; PubMed=8706697;
RA Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I.,
RA Ek B., Larsson M., Juhlin C., Hellman P., Davis H., Akerstroem G.,
RA Rask L., Morse B.;
RT "Cloning and sequencing of human gp330, a Ca(2+)-binding receptor
RT with potential intracellular signaling properties.";
RL Eur. J. Biochem. 239:132-137(1996).
RN [2]
RP SEQUENCE OF 2705-4453 FROM N.A.
RC TISSUE=Kidney;
RA Knaak C., Argraves W.S.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3833-4453 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95048397; PubMed=7959795;
RA Korenberg J.R., Argraves K.M., Chen X.N., Tran H.,
RA Strickland D.K., Argraves W.S.;
RT "Chromosomal localization of human genes for the LDL receptor family
RT member glycoprotein 330 (LRP2) and its associated protein RAP
RT (LRPAP1).";
RL Genomics 22:88-93(1994).
RN [4]
RP SEQUENCE OF 4139-4406 FROM N.A.
RX MEDLINE=94244704; PubMed=8187828;
RA Lundgren S., Hjaelm G., Hellman P., Ek B., Juhlin C., Rastad J.,
RA Klarekog L., Akerstrom G., Rask L.;
RT "A protein involved in calcium sensing of the human parathyroid and
RT placental cytotrophoblast cells belongs to the LDL-receptor protein
RT superfamily.";
RL Exp. Cell Res. 212:344-350(1994).
RN [5]
RP FUNCTION.
RX MEDLINE=95286588; PubMed=7768901;
RA Kounnas M.Z., Loukinova E.B., Stefanosson S., Harmony J.A.K.,
RA Brewer B.H., Strickland D.K., Argraves W.S.;
RT "Identification of glycoprotein 330 as an endocytic receptor for
RT apolipoprotein J/clusterin.";
RL J. Biol. Chem. 270:13070-13075(1995).
CC -!- FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY, BUT
CC ALSO LIGANDS IN COMMON WITH OTHER FAMILY MEMBERS: PLASMINOGEN,
CC EXTRACELLULAR MATRIX COMPONENTS, PLASMINOGEN ACTIVATOR-PLASMINOGEN
CC ACTIVATOR INHIBITOR TYPE I COMPLEX, APOLIPOPROTEIN E-ENRICHED
CC BETA-VLDL, LIPOPROTEIN LIPASE, LACTOFERRIN AND CALCIUM.
CC -!- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS
CC APROTININ, AMINOGLYCOSIDES AND POLYMYXIN B (BY SIMILARITY).
CC -!- FUNCTION: MAY PARTICIPATE IN REGULATION OF PARATHYROID-HORMONE AND
CC PARA-THYROID-HORMONE-RELATED PROTEIN RELEASE.
CC -!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
CC ASSOCIATED PROTEIN (RAP).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL
CC PROXIMAL TUBULES.
CC -!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
CC -!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; U33837; AAB41649.1; -.
DR EMBL; U04441; AAB02882.1; -.
DR EMBL; S73145; AAB30825.1; -.
DR HSSP; P01130; 1AJJ.
DR MIM; 600073; -.
DR InterPro; IPR000033; -.
DR InterPro; IPR000152; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR001881; -.
DR InterPro; IPR002172; -.
DR Pfam; PF00008; EGF_13.
DR Pfam; PF00057; ldl_recept_a; 36.
DR Pfam; PF00058; ldl_recept_b; 37.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01209; LDLRA_1; 31.
DR PROSITE; PS00068; LDLRA_2; 36.
KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;
KW Receptor; EGF-like domain; Signal; Polymorphism.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 4655 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
FT DOMAIN 26 4423 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 4424 4446 POTENTIAL.
FT DOMAIN 4447 4655 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 105 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 106 144 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 145 181 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 182 219 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 220 258 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 264 308 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 309 347 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 348 386 EGF-LIKE 1.
FT DOMAIN 436 477 EGF-LIKE 2.
FT DOMAIN 479 520 LDL-RECEPTOR CLASS B 1.
FT DOMAIN 522 567 LDL-RECEPTOR CLASS B 2.
FT DOMAIN 569 612 LDL-RECEPTOR CLASS B 3.
FT DOMAIN 613 653 LDL-RECEPTOR CLASS B 4.
FT DOMAIN 659 705 EGF-LIKE 3.
FT DOMAIN 753 794 LDL-RECEPTOR CLASS B 6.
FT DOMAIN 796 836 LDL-RECEPTOR CLASS B 7.
FT DOMAIN 838 880 LDL-RECEPTOR CLASS B 8.
FT DOMAIN 882 924 LDL-RECEPTOR CLASS B 9.
FT DOMAIN 970 1014 EGF-LIKE 4.
FT DOMAIN 1024 1062 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 1065 1103 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 1107 1145 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 1147 1185 LDL-RECEPTOR CLASS A 11.
FT DOMAIN 1186 1224 LDL-RECEPTOR CLASS A 12.
FT DOMAIN 1228 1268 LDL-RECEPTOR CLASS A 13.
FT DOMAIN 1269 1307 LDL-RECEPTOR CLASS A 14.
FT DOMAIN 1310 1350 LDL-RECEPTOR CLASS A 15.
FT DOMAIN 1349 1389 EGF-LIKE 5.
FT DOMAIN 1429 1478 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1478 1519 LDL-RECEPTOR CLASS B 10.
FT DOMAIN 1521 1562 LDL-RECEPTOR CLASS B 11.
FT DOMAIN 1566 1608 LDL-RECEPTOR CLASS B 12.
FT DOMAIN 1610 1653 LDL-RECEPTOR CLASS B 13.
FT DOMAIN 1655 1695 LDL-RECEPTOR CLASS B 14.
FT DOMAIN 1700 1741 EGF-LIKE 7.
FT DOMAIN 1790 1831 LDL-RECEPTOR CLASS B 15.
FT DOMAIN 1833 1881 LDL-RECEPTOR CLASS B 16.
FT DOMAIN 1883 1929 LDL-RECEPTOR CLASS B 17.
FT DOMAIN 1931 1971 LDL-RECEPTOR CLASS B 18.
FT DOMAIN 1972 2012 LDL-RECEPTOR CLASS B 19.
FT DOMAIN 2018 2059 EGF-LIKE 8.
FT DOMAIN 2107 2155 LDL-RECEPTOR CLASS B 20.
FT DOMAIN 2157 2200 LDL-RECEPTOR CLASS B 21.

FT	DOMAIN	2202	2244	LDL-RECEPTOR CLASS B 22.
FT	DOMAIN	2246	2288	LDL-RECEPTOR CLASS B 23.
FT	DOMAIN	2290	2331	LDL-RECEPTOR CLASS B 24.
FT	DOMAIN	2342	2383	EGF-LIKE 9.
FT	DOMAIN	2431	2476	LDL-RECEPTOR CLASS B 25.
FT	DOMAIN	2478	2517	LDL-RECEPTOR CLASS B 26.
FT	DOMAIN	2519	2561	LDL-RECEPTOR CLASS B 27.
FT	DOMAIN	2563	2603	LDL-RECEPTOR CLASS B 28.
FT	DOMAIN	2604	2646	LDL-RECEPTOR CLASS B 29.
FT	DOMAIN	2651	2693	EGF-LIKE 10.
FT	DOMAIN	2698	2738	LDL-RECEPTOR CLASS A 16.
FT	DOMAIN	2739	2777	LDL-RECEPTOR CLASS A 17.
FT	DOMAIN	2778	2819	LDL-RECEPTOR CLASS A 18.
FT	DOMAIN	2820	2861	LDL-RECEPTOR CLASS A 19.
FT	DOMAIN	2862	2901	LDL-RECEPTOR CLASS A 20.
FT	DOMAIN	2904	2945	LDL-RECEPTOR CLASS A 21.
FT	DOMAIN	2946	2990	LDL-RECEPTOR CLASS A 22.
FT	DOMAIN	2991	3029	LDL-RECEPTOR CLASS A 23.
FT	DOMAIN	3030	3070	LDL-RECEPTOR CLASS A 24.
FT	DOMAIN	3073	3110	LDL-RECEPTOR CLASS A 25.
FT	DOMAIN	3111	3151	EGF-LIKE 11.
FT	DOMAIN	3152	3192	EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	3239	3280	LDL-RECEPTOR CLASS B 30.
FT	DOMAIN	3282	3331	LDL-RECEPTOR CLASS B 31.
FT	DOMAIN	3333	3375	LDL-RECEPTOR CLASS B 32.
FT	DOMAIN	3377	3418	LDL-RECEPTOR CLASS B 33.
FT	DOMAIN	3419	3459	LDL-RECEPTOR CLASS B 34.
FT	DOMAIN	3465	3509	EGF-LIKE 13.
FT	DOMAIN	3510	3550	LDL-RECEPTOR CLASS A 26.
FT	DOMAIN	3551	3591	LDL-RECEPTOR CLASS A 27.
FT	DOMAIN	3592	3632	LDL-RECEPTOR CLASS A 28.
FT	DOMAIN	3633	3673	LDL-RECEPTOR CLASS A 29.
FT	DOMAIN	3676	3716	LDL-RECEPTOR CLASS A 30.
FT	DOMAIN	3717	3756	LDL-RECEPTOR CLASS A 31.
FT	DOMAIN	3757	3795	LDL-RECEPTOR CLASS A 32.
FT	DOMAIN	3796	3834	LDL-RECEPTOR CLASS A 33.
FT	DOMAIN	3840	3880	LDL-RECEPTOR CLASS A 34.
FT	DOMAIN	3881	3922	LDL-RECEPTOR CLASS A 35.
FT	DOMAIN	3926	3964	LDL-RECEPTOR CLASS A 36.
FT	DOMAIN	3966	4006	EGF-LIKE 14.
FT	DOMAIN	4007	4048	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	4154	4195	LDL-RECEPTOR CLASS B 35.
FT	DOMAIN	4197	4239	LDL-RECEPTOR CLASS B 36.
FT	DOMAIN	4242	4282	LDL-RECEPTOR CLASS B 37.
FT	DOMAIN	4330	4368	EGF-LIKE 16.
FT	DOMAIN	4377	4411	EGF-LIKE 17.
Query Match 2.5%; Score 123; DB 1; Length 4655;				
Best Local Similarity 16.8%; Pred. No. 3.2;				
Matches 189; Conservative 118; Mismatches 303; Indels 516; Gaps 54;				
QY	25	CLGFTAHRKRAEGW	-----EEGPTVLSDSPWTNISGCKGRFELQE-----	68
Db	1200	CIGVT	-----NRCDGVFDCSDNSDEAGCP-----TRPPGMCHSDEFQCQEDGICIPNF	1247
QY	69	---AGPPDC	-----RCNLCCKSYTSCCHDFDELCLKTARGWECTK	105
Db	1248	WECGHPDCLYGSDEHNACVPKTCPSYFHCDN	-----GNCIH-----RAWLCDR	1292
QY	106	DR-CGEVRNEENA	---CHCSE---DCLARGDCCTNYQVCKG-----	ESHWVD-D 147
Db	1293	DNDGDMSEKDCPTQFRCPSWQQLGH-NICVNLVSVCDGIFDCPNGTDESPLCNGN	1351	
QY	148	DCEEIKA	-----AECPAGFVRPPLIIFSVVDGFRASYMKKGSKVMPNIEK--	191
Db	1352	SCSDFNGGCTHECVQEPFGAKCLPLGLF	-----LANDSKTCEDIDECD	1395
QY	192	-LRSCGTHSPYMRPVY	-----	PTKTF 211
Db	1396	ILGSCSQHCYNMRGSRFCSDTGYMLESdgRTCKVTASESLLLLVASQNKIIADSVTSQV	1455	
QY	212	PNLYTLA-TGLY	---PESHGIVGNSMYDP-----VFDFTLHR---	245

Db	1456	HNIYSLVENGSIYIVAVDFDSISGRIFWSDATQGTWSAFQNGTDRRVVFDSSIIILTETIA		1511
QY	246	----GREKF-----NHR-----	-----W-WGG	257
Db	1516	IDWVGRNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPRMNEHLLFWSDWGH	-----	1575
QY	258	QPLWITATKQG-----VKAGTFFW--SVVIPHERRIILTLRWLTLPDHERPSVYAFYSEQ	-----	310
Db	1576	HPRIERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFM-----DSYLDYMDF	-----	1624
QY	311	PDFSGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQ-----	-----ERPVA	353
Db	1625	CDYNGH-----HRRQVIASDLIRHPYALTTFEDSVY	-----	1656
QY	354	PPKRRRKIHRMDHYAAETRODKMTN--PLREIDKIVGQLMDGLKQLKLRRCVNVIFVG	-----	410
Db	1657	WTDRASTRVMRANKWHGNGQSVVMYNIQWPLGIVAVHPSKQPNVNPCAFSRCSHLCILS	-----	1716
QY	411	DHGMEDVTC-----DRTEFL-----	-----	425
Db	1717	SQGFHYSCVCPGWSLSPDLLNCLRDDQPFLLTVROHIIFGISLNEVKNSDAMVPIAG	-----	1776
QY	426	-----SNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHF	-----	473
Db	1777	IQGLDVEFDAAEQYIYVEN--PGEIHRVKTDGTN-----RTVFASISMVGPSMNL	-----	1826
QY	474	K-PYLKQHLPKRLHYANNRRIEDIHLV-----ERRHWVARK-----PLDVYKKPS	-----	518
Db	1827	ALDWISRNL-----YSTNPRQTSIEVLTLHGDIRYKRTLIANDGTALGVGFPIGITVDPA	-----	1881
QY	519	GKCFEQGDHGFDNKV-----NSMQTVFVGYPGTFKYKTKVPPFENIELYNVMCD	-----	567
Db	1882	RKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTG-----NLE--HLECV	-----	1924
QY	568	LLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPG---IMYLSQDSDLGCTCDD	-----	623
Db	1925	TLDIEE-----QKLYWAVTGRGV---IERGNVDGTDRLMLVHQLSHPWGIAVHD	-----	1970
QY	624	KVEPKNKLDLNLKRLHTKGTSTEEHLLYGRPAVLYRT--RYDILYHTDFESGYSEIFL--	-----	679
Db	1971	-----SFLYTDQEYEVIERVDKATGANKIVLRD	-----	1999
QY	680	----MLLWTSYTVSKQAEVSS-----VPDHLTSCVRPDVVRVSPFSQNCCL	-----	720
Db	2000	NVPNLRGLQVYHRRNAAESSNGCSNNMNACQICLPVPGGLFSCA-----	-----	2044
QY	721	AYKNDKQMSYGF-LFPPYLSSSPEAKYDAFLVTNMVPMVPAFKRWVNYFORVLVKKYASE	-----	779
Db	2045	-----CATGFKLNPDNRSCLP---YNSFIVVSMLSAIRGFSLELSDHSETMVPVAGQG	-----	2094
QY	780	RNG-----VNVISGPIFDYDGLHDTEDKIKQY-VEGSSI-PVPTH	-----	819
Db	2095	RNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTH	-----	2140
RESULT 8				
LT23_CAEEL				
ID	LT23_CAEEL	STANDARD;	PRT;	1323 AA.
AC	P24348;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	LET-23 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112).			
GN	LET-23 OR KIN-7 OR ZKI067.1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91080919; Pubmed=1979659;			
RA	Aroian R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg P.W.;			
RT	"The let-23 gene necessary for Caenorhabditis elegans vulval			

RT induction encodes a tyrosine kinase of the EGF receptor subfamily.";

RL Nature 348:693-699(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=96177760; PubMed=8604137;

RA Sakai T., Koga M., Ohshima Y.;

RT "Genomic structure and 5' regulatory regions of the let-23 gene in

RT the nematode C. elegans.";

RL J. Mol. Biol. 256:548-555(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Thomas K.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP MUTANTS.

RX MEDLINE=94147981; PubMed=8313880;

RA Aroian R.V., Les G.M., Sternberg P.W.;

RT "Mutations in the Caenorhabditis elegans let-23 EGFR-like gene define

RT elements important for cell-type specificity and function.";

RL EMBO J. 13:360-366(1994).

CC -!- FUNCTION: TYROSINE KINASE RECEPTOR REQUIRED FOR THE INDUCTION OF

CC C.ELEGANS VULVA. POSSIBLE RECEPTOR FOR THE INDUCTIVE SIGNAL

CC REQUIRED FOR VULVAL DEVELOPMENT. ACTIVATED BY LIN-3 AND ACTS BY

CC WAY OF LET-60 RAS. THE LIN-3/LET-23 PAIR IS A SIMPLIFIED VERSION

CC OF THE MAMMALIAN NEUREGULIN-ERBB NETWORK.

CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

CC PROTEIN TYROSINE PHOSPHATE.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X57767; CAA40919.1; ALT_SEQ.

DR EMBL; D63426; BAA09729.1; ALT_INIT.

DR EMBL; Z70038; CAA93882.1; -.

DR PIR; S13422; S13422.

DR HSSP; P11362; 1FGI.

DR WormPep; ZK1067.1; CE03840.

DR InterPro; IPR000494; -.

DR InterPro; IPR000719; -.

DR InterPro; IPR001245; -.

DR InterPro; IPR002174; -.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF01030; Recep_L_domain; 2.

DR Pfam; PF00069; pkinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

DR Transmembrane; Glycoprotein; Receptor; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 1323 LET-23 RECEPTOR PROTEIN-TYROSINE KINASE.

FT DOMAIN 23 818 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 819 841 POTENTIAL.

FT DOMAIN 842 1323 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 885 1152 PROTEIN KINASE.

FT NP_BIND 891 899 ATP (BY SIMILARITY).

FT BINDING 919 919 ATP (BY SIMILARITY).

FT ACT_SITE 1010 1010 BY SIMILARITY.

FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 655 655 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	776	776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	368	368	C -> Y (IN SY10).
FT	VARIANT	469	469	G -> R (IN MN216).
FT	VARIANT	700	700	C -> W (IN MN23).
FT	VARIANT	753	753	C -> Y (IN SY11).
FT	VARIANT	1065	1065	T -> I (IN SY16).
FT	VARIANT	1074	1074	G -> E (IN SY7).
SQ	SEQUENCE	1323 AA;	150510 MW;	6B0307EE53EEFA99 CRC64;

Query Match 2.4%; Score 122; DB 1; Length 1323;
Best Local Similarity 18.4%; Pred. No. 0.73;
Matches 149; Conservative 106; Mismatches 290; Indels 264; Gaps 43;

QY	48	SDSPWNTISGSK	-----GRCFELQEAAGPPDCRDNLC-----KSYTSCC	87
Db	225	NDKCWGSNDNCQRVRSVCPKSCSQCFYSNSTSSYEC	-CDSACLGCGTGHGPKNCIACS	283
QY	88	-HDFELCLKTARGWECTKDRCEV	-----RNEENACHCSEDC-----LARGDCCTNYQVV	137
Db	284	KYELDGICIEETCPSRKIFNHTKTRLVFNPDGRYQNGNHCVCPELLIENDVCVRH	---340	
QY	138	CKGESHV-VDD--DCEEIKAAECAGFVRPPLIIFSVDGFRASYMKKSGSKVMPNIEKL	R	193
Db	341	CSDGHYDATKDVRECEKCRSSCPK	-----ICTVDGHLT-----NETLKNLEGE	386
QY	194	SCGTHSPYMRPVYPTKTFPNLYTLAT	-GLYPESHGIVGNSMYDPVFDATEFH-LRGREKFN	251
Db	387	QIDGH---LIEHAFTYEQLKVLETVKIVSEYITIVQNFYDLKFLKNLQIIEGRKLHN	442	
QY	252	HRWGG-----QPLWITATKQGVKAGTFFWSVVIPIHERRILITILRWLTLPDHERPSVY	304	
Db	443	VRWALIQDDLEELSLNLSKL-ITKG	-----AVLIMKNHRLC-----480	
QY	305	AFYSEQPDFSGHKYGPFGPEESSYSGSPPTAKRPKRKVAPKRQRPVAPPKRRRIHR	364	
Db	481	--YVSKIDWSS-----IITSKGDNKPKSLAIAENR-----508		
QY	365	MDHYAAETRDQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEF	424	
Db	509	-DSKLCETE	-----RVCDK-----NCNKRGCWGKEPEDCLECKT	542
QY	425	LSNYLTNVDDITLVPGLGRIRSKFSNNA-KYDPKAIAN	-----LTCKKPDQHFQPY	476
Db	543	WKSVGTCVEKC---DTKGLRNTQSMKERCSPCECTCNGLGELDCLTRH	-----590	
QY	477	LKQHLPKRLHYAN-NRRIEDIHLLVERRWVHVARCKPL--DVYKKPSGCKFFQGDHGFQDNKV	533	
Db	591	-----KTLYNSDFGNRMECVH-----DCPVSHFPTQKNVCEKCHPTCYDNGCTGPDNSN	638	
QY	534	NSMQTVFVGYG--PTFKYTKVPPFENIELY	-----NVMC---DL-----568	
Db	639	-----LGYGGCKQCKYAVK---YENDTIFCLQSSGMNNVCVENDLPNYIYSTYDTEGV	688	
QY	569	-----LGLKPAPNNGTHGSLNHLRLTNT-FRPTMPEEVTRPNYPGIMVYLSQDFD--	616	
Db	689	IETHCEKCSISCKTCSSAGRNWVQNKVCVKHVEYQPNPSEICMDQCPVNSFWVPDNTNT	748	
QY	617	-----LGC-TCDD-----KVEPKNKLDELNKLRLHTKGSTEERHLLY	651	
Db	749	VCKKCHHECDQNYHCANGQSTGCQCKCKNETVFKGDIAQCVCSECPKLPFSNPANGECIDY	808	
QY	652	GRPAVLRYTRYDILYHTDFESGYSEIFMLL--- <td>708</td> <td></td>	708	
Db	809	DIASRQRKTRMVIIGSVLF--GFVAVMFLFILLVYWRQCRIGKKLKLKIAEMVD-MPELTPIID	865	
QY	709	VRVSPFSQNC-----LAYKNDKQMSYG	731	
Db	866	ASVRPNMSRICLIPSELOTKLDKKLKLGAG	894	

RESULT 9

QY 703 SCVRPDVRSFSONCLAYKNDQMSYGFLEP--PYLSSSPEAKYDAFLVTNMVMP- 759
Db 61 FKEDPDV--PSLFRSTLADYSGSGFDRGHMAPAGDAVATQP-AMDQTFYLSNMSPOVGI 116
QY 760 AFKR-VWNY---FQRLVKKYASERNGVNVISGPIF--DYDYDGLHDTEDKIKQVVEGSS 813
Db 117 GFNRHYWAYLEGFCRSLTKKFS- ---VYVFTGPLELPTKSGDGKTYTVYTNVLQ-----GN 168
QY 814 IPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMK 873
Db 169 VAVPTHFYKVL-----VPQGDKNKYAYGAFILP-----NQAID-----TKTFLT 207
QY 874 MHTARVRDIEHLTSLDFFRK 893
Db 208 NEKVKLT DVEKASGLTFFDK 227

RESULT 11
VTNC_RABIT
ID VTNC_RABIT STANDARD; PRT; 475 AA.
AC P22458;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN)
DE (GLYCOPROTEIN 66).
GN VTN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RX MEDLINE=91065939; PubMed=1701177;
RA Sato R., Komine Y., Imanaka T., Takano T.;
RT "Monoclonal antibody EMR1a/212D recognizing site of deposition of
RT extracellular lipid in atherosclerosis. Isolation and
RT characterization of a cDNA clone for the antigen."
RL J. Biol. Chem. 265:21232-21236(1990).
CC -!- FUNCTION: VITRONECTIN IS A CELL ADHESION AND SPREADING FACTOR
CC FOUND IN SERUM AND TISSUES. VITRONECTIN INTERACT WITH
CC GLYCOSAMINOGLYCANS AND PROTEOGLYCANS. IS RECOGNIZED BY CERTAIN
CC MEMBERS OF THE INTEGRIN FAMILY AND SERVES AS A CELL-TO-SUBSTRATE
CC ADHESION MOLECULE. INHIBITOR OF THE MEMBRANE-DAMAGING EFFECT OF
CC THE TERMINAL CYTOLYTIC COMPLEMENT PATHWAY.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: CONTAINS 2 HEMOPEXIN-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M55442; AAA31258.1; --
DR PIR; A38340; A38340.
DR HSSP; P45452; IPEX.
DR InterPro; IPR000585; --
DR InterPro; IPR001212; --
DR Pfam; PF01033; Somatomedin_B; 1.
DR Pfam; PF00045; hemopexin; 4.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00024; HEMOPEXIN; 2.
DR PROSITE; PS00524; SOMATOMEDIN_B; 1.
KW Heparin-binding; Cell adhesion; Glycoprotein; Sulfatation; Signal.
FT SIGNAL 1 19
FT CHAIN 20 475 VITRONECTIN.

FT DOMAIN 20 63 SOMATOMEDIN-B LIKE.
FT DOMAIN 150 287 HEMOPEXIN-LIKE 1.
FT DOMAIN 288 475 HEMOPEXIN-LIKE 2.
FT DOMAIN 366 392 GLYCOSAMINOGLYCAN BINDING REGION.
FT SITE 64 66 CELL ATTACHMENT SITE.
FT MOD_RES 75 75 SULFATATION (BY SIMILARITY).
FT MOD_RES 78 78 SULFATATION (BY SIMILARITY).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 475 AA; 53943 MW; D5D1F31B8C2FA12D CRC64;

Query Match 2.4%; Score 119.5; DB 1; Length 475;
Best Local Similarity 23.1%; Pred. No. 0.29;
Matches 118; Conservative 50; Mismatches 195; Indels 147; Gaps 30;

QY 46 VLSDSPWNTNISGCKGRCFELQEAAGPPDCRDNLCCKSYTSCCHDFDELCL-KTARG---- 100
Db 17 VLADQE-----SCKDRCTEGFNAN-RKCQDELCSYYQSCCADYAAECKPQVTRGDVFT 69
QY 101 -----WECTKDRCGEVRNEENAC-----HCSEDCIARGDCCTNYQVVCKGESHW 144
Db 70 MPEDEYGPYDIEQTKDNASVHAQPESPTVGQPTLSPDLQTEGGAAPTHTHEVPLEPEMET 129
QY 145 VDDDCETKAAECPAGFVRPP-----LIIFSVDGFRASYMKK--GSKVM 186
Db 130 LRPEGEDLQAGTTELGTSSAPAEELCSCKPFDATDLKNGSLFAFRGQYCYELDETAVR 189
QY 187 PNIEKLS--CGTHSP-----YMRPVYPTKTF-----PNLYTLATGL-----YPE--SHGIVG 230
Db 190 PGYPKLIQDVWVGIEGPIDAAFTTRINCOGKTYLFKGSQYWRFFEDGILDPDYPRNISEGFSG 249
QY 231 NSMYDPVFDATFHL-----RGREKFNHRWGGQPLWITATKQ-----GVKAGTFFWS 277
Db 250 --IPDNV-DAAFALPAHSYSGRERV--YFFKGDKYWEYQFQQPSQEECEGSSLSAVFEH 304
QY 278 VVIPHE---RRILTLRLWTLTPDHERPSVYAFYSEQPDF-SGHKYGPFPGPEESS-----Y 328
Db 305 FAMLHRDSWEDIFKLLF-----GRPSGGA---RQPQFISRDWHGVPGKVDAAMAGRIY 355
QY 329 GSPETPAKRPKRKVAPKRRQERPVPAPKKRRKRIHRMDHYAAETRODKMTNPLREIDKIV 388
Db 356 ISGLTPSPSAKKQ-----KSRRSRKR--YRSRYGHRSQNS-RRLRSR 397
QY 389 GQLMDGLKQLKLRRCNVIFVGDHGMEDVTCRTEFLSNLYLTNVDITLVPGTLGRIRSK 448
Db 398 SRLWFSSEEVSL-----GPYNYED-----YETS-----WLKPATSEPIQSV 433
QY 449 --FSNNAKYDPKAIIANLTCKKPDQHEKPY 476
Db 434 YFFSGDKYR-----VNLRTQRVDTVNPY 458

RESULT 12
NUCL_SCHPO
ID NUCL_SCHPO STANDARD; PRT; 335 AA.
AC Q10480;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROBABLE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
GN SPAC17C9.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Murphy L., McDougall R., Jones L., Simpson I., McNeill A., Harris D.,
RA Barrell B.G., Rajandream M.A., Walsh S.V.;

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 870 870 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1394 AA; 152791 MW; DFFCA81A40B2C7D1 CRC64;

Query Match 2.2%; Score 112; DB 1; Length 1394;
Best Local Similarity 23.8%; Pred. No. 4.1;
Matches 49; Conservative 17; Mismatches 48; Indels 92; Gaps 15;

QY 44 PTVLSDSPWTNIGS-----C-----KGRCFELQEAAGPPD-CR---CDNLCKSYTSCC 87
Db 678 PSTCPDEQCVNSPGSYQCVPCTEGFRGWNQCCLDVDECLEPNVCANGDCSNLEGSYMCSC 737

QY 88 H-----DFDEL-----CLKTARGWECT-----KDRC----- 108
Db 738 HKGYTRTPDHKHCRIDECQQGNLVCNGQCKNTEGFRCTCGQGYQLSAAKQCEIDDEC 797

QY 109 -----GEVRNEENA-----C-----HCSE--DCL-----ARGDCCT---NY 134
Db 798 QHRHLCAHGQCRNTEGFSQCQGYRASGLGDHCEINEDKSKVCQRCGDCINTAGSY 857

QY 135 QVVKGESHWVDDD--CEEIKAACEP 158
Db 858 DCTCP-DGFQLDDNKTQDINECEHP 882

RESULT 15
NUCG_BOVIN STANDARD; PRT; 299 AA.
AC P38447;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).
GN ENDOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93342514; PubMed=7688144;
RA Cote J., Ruiz-Carrillo A.;
RT "Primers for mitochondrial DNA replication generated by endonuclease
G.";
RL Science 261:765-765(1993).
RN [2]
RP SEQUENCE OF 49-75.
RC TISSUE=Liver, and Thymus;
RX MEDLINE=88198128; PubMed=3360771;
RA Moos M. Jr., Nguyen N.Y., Liu T.-Y.;
RT "Reproducible high yield sequencing of proteins electrophoretically
separated and transferred to an inert support.";
RL J. Biol. Chem. 263:6005-6009(1988).
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Heart;
RX MEDLINE=95175374; PubMed=7870594;
RA Gershenson M., Houmiel K.L., Low R.L.;
RT "Endonuclease G from mammalian nuclei is identical to the major
endonuclease of mitochondria.";
RL Nucleic Acids Res. 23:88-97(1995).
CC -!- FUNCTION: CLEAVES DNA AT DOUBLE-STRANDED (DG)N.(DC)N AND AT
CC SINGLE-STRANDED (DC)N TRACTS. IN ADDITION TO DEOXYRIBONUCLEASE
CC ACTIVITIES, ALSO HAS RIBONUCLEASE (RNASE) AND RNASE H ACTIVITIES.
CC CAPABLE OF GENERATING THE RNA PRIMERS REQUIRED BY DNA POLYMERASE
CC GAMMA TO INITIATE REPLICATION OF MITOCHONDRIAL DNA.
CC -!- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.

CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X72802; CAA51320.1; -.
CC InterPro; IPR001604; -.
CC Pfam; PF01223; Endonuclease; 1.
CC PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
KW Hydrolase; Nuclease; Endonuclease; Mitochondrion; Transit peptide;
KW Magnesium.
FT TRANSIT 1 48 MITOCHONDRION.
FT CHAIN 49 299 ENDONUCLEASE G.
FT ACT_SITE 143 143 BY SIMILARITY.
FT CONFLICT 172 172 H -> S (IN REF. 3; PROBABLE ERROR).
FT CONFLICT 264 264 H -> S (IN REF. 3; PROBABLE ERROR).
SQ SEQUENCE 299 AA; 32261 MW; B28FAFF56F04CFC7 CRC64;

Query Match 2.2%; Score 111.5; DB 1; Length 299;
Best Local Similarity 25.8%; Pred. No. 0.6;
Matches 32; Conservative 24; Mismatches 41; Indels 27; Gaps 6;

QY 741 SPEAKYDAFLVTNMVMPYPAF-KRVWN---YFQRLVKKYASERNGVNVISGPIFDYD 796
Db 153 SQKAMDDTFYLSNVAPQVPHLNONAWNLEKYSRLTRY-----QNVYVCTGPLF----- 203

QY 797 GLHDTEDKIKQYVE-----GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHR 851
Db 204 -LPRTADGKSYVKYQVIGKNHVAVPTHFFKVL-----LEAAGGQIELRSYVMPNA 254

QY 852 PDNE 855
Db 255 PVDE 258

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:57 ; Search time 42.51 Seconds
(without alignments)
2847.779 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSQIISLFTFAV.....RSYPEILTLKTYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues 425026

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5019	100.0	915	4 Q13827	Q13827 homo sapien
2	4681	93.3	863	4 Q13822	Q13822 homo sapien
3	4666	93.0	863	4 Q15117	Q15117 homo sapien
4	4439.5	88.5	862	11 Q9R1E6	Q9r1e6 mus musculu
5	4306	85.8	885	11 Q64610	Q64610 rattus norv
6	2084	41.5	875	11 Q63490	Q63490 rattus norv
7	2084	41.5	875	11 P97676	P97676 rattus norv
8	2081	41.5	875	11 P97675	P97675 rattus norv
9	2057.5	41.0	876	11 P70641	P70641 rattus norv
10	2040.5	40.7	875	4 O14638	O14638 homo sapien
11	1955.5	39.0	845	4 Q9NP23	Q9np23 homo sapien
12	1955.5	39.0	925	4 Q9P1P6	Q9p1p6 homo sapien
13	1151	22.9	817	14 Q90761	Q90761 fowlpox vir
14	1151	22.9	817	14 Q9J5H1	Q9j5h1 fowlpox vir
15	646.5	12.9	457	10 Q9SU82	Q9su82 arabidopsis
16	613	12.2	479	10 Q9FS13	Q9fs13 spinacia ol
17	612	12.2	496	10 Q9SU83	Q9su83 arabidopsis
18	611.5	12.2	479	10 Q42974	Q42974 oryza sativ
19	610	12.2	829	5 P90754	P90754 caenorhabdi

20	609	12.1	461	10 Q9SU81	Q9su81 arabidopsis
21	539.5	10.7	485	3 Q94323	Q94323 schizosacch
22	534	10.6	251	4 Q9NQM9	Q9nqm9 homo sapien
23	526.5	10.5	257	11 O88827	O88827 rattus norv
24	522	10.4	429	2 O69013	O69013 zymomonas m
25	512	10.2	453	4 Q9Y6X5	Q9y6x5 homo sapien
26	474.5	9.5	477	11 Q9EQG7	Q9eqg7 mus musculu
27	466.5	9.3	477	4 Q9UJA9	Q9uja9 homo sapien
28	461	9.2	433	2 Q9PAB9	Q9pab9 xylella fas
29	456.5	9.1	674	5 P90755	P90755 caenorhabdi
30	427	8.5	152	4 Q9H515	Q9h515 homo sapien
31	394.5	7.9	281	6 Q9TSB2	Q9tsb2 bos taurus
32	309.5	6.2	151	11 Q9QYV2	Q9qyv2 rattus norv
33	297.5	5.9	614	5 Q17540	Q17540 caenorhabdi
34	241.5	4.8	133	10 Q9SU80	Q9su80 arabidopsis
35	238	4.7	453	5 Q22129	Q22129 caenorhabdi
36	234	4.7	45	4 Q14555	Q14555 homo sapien
37	171	3.4	385	13 Q9PTU6	Q9ptu6 paralichthy
38	170.5	3.4	44	11 Q9R1D5	Q9r1d5 mus musculu
39	163	3.2	360	5 O45359	O45359 caenorhabdi
40	158.5	3.2	1054	11 Q9JM99	Q9jnm9 mus musculu
41	145.5	2.9	465	2 O69954	O69954 streptomyce
42	142	2.8	1186	14 O55767	O55767 chilo iride
43	135	2.7	32	6 Q9TRD2	Q9trd2 bos taurus
44	134	2.7	1404	4 Q92954	Q92954 homo sapien
45	132	2.6	462	2 Q9Z4Z4	Q9z4z4 streptomyce

ALIGNMENTS

RESULT	1
Q13827	
ID	Q13827
AC	Q13827
PT	Q1-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	AUTOTAXIN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=TUMOR;
RX	MEDLINE=95074054; PubMed=7982964;
RA	Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA	Sobel M.E., Liotta L.A., Stracke M.L.;
RT	"cDNA cloning of the human tumor motility-stimulating protein,
RT	autotaxin, reveals a homology with phosphodiesterases."
RL	J. Biol. Chem. 269:30479-30484(1994).
DR	EMBL; L35594; AAA64785.1; -
DR	InterPro; IPR001212; -
DR	InterPro; IPR001604; -
DR	InterPro; IPR002591; -
DR	Pfam; PF01033; Somatomedin_B; 2.
DR	Pfam; PF01663; Phosphodiester; 1.
DR	PRINTS; PR00022; SOMATOMEDINB.
DR	PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR	SMART; SM00477; NUC; 1.
SQ	SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;

Query Match	100.0%;	Score	5019;	DB	4;	Length	915;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	915;	Conservative	0;	Mismatches	0;	Indels	0;
		Gaps	0;				
QY	1	MARRSSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEGPPTVLSDSPWTNIGSGCK	60				
Db	1	MARRSSFQSQIISLFTFAVGVSICLGFTAHRIKRAEGWEGPPTVLSDSPWTNIGSGCK	60				
QY	61	GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC	120				

```
Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCTNYQVWCKGESHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCTNYQVWCKGESHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
QY 181 KGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPDHER 300
Db 241 TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQERPVPAPKKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQERPVPAPKKRRR 360
QY 361 KIHRRMDHYAAETRQDKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
Db 361 KIHRRMDHYAAETRQDKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
QY 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
QY 481 LPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
Db 481 LPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
QY 541 VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTRPTMPEEV 600
QY 601 TRPNYPGIMYLQSDFDLCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGRPAVLYRT 660
Db 601 TRPNYPGIMYLQSDFDLCTCDDKVEPKNKLDLNLKRLHTKGSTEERHLLYGRPAVLYRT 660
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNC 720
QY 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKYASER 780
Db 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKYASER 780
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSSRYPE 900
Db 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSSRYPE 900
QY 901 ILTLKTYLHYESEI 915
Db 901 ILTLKTYLHYESEI 915
```

RESULT 2
Q13822

```
ID Q13822 PRELIMINARY; PRT; 863 AA.
AC Q13822;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE AUTOTAXIN-T.
GN ATX-T.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "CDNA cloning of the human tumor motility-stimulating protein,
RL autotaxin, reveals a homology with phosphodiesterases.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96158950; PubMed=8579579;
RA Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,
RA Manrow R.E., Liotta L.A., Stracke M.L.;
RT "Cloning, chromosomal localization, and tissue expression of autotaxin
RL from human teratocarcinoma cells.";
RL Biochem. Biophys. Res. Commun. 218:714-719(1996).
DR EMBL; L46720; AAB00855.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BABC CRC64;
```

Query Match 93.3%; Score 4681; DB 4; Length 863;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 858; Conservative 2; Mismatches 3; Indels 52; Gaps 1;

```
QY 1 MARRSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEGPPTVLSDSPWNTNISGSK 60
Db 1 MARRSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEGPPTVLSDSPWNTNISGSK 60
QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCTNYQVWCKGESHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCTNYQVWCKGESHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
QY 181 KGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPDHER 300
Db 241 TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQERPVPAPKKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYSGSPTPAKRPKRKVAPKRRQERPVPAPKKRRR 360
QY 361 KIHRRMDHYAAETRQDKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
Db 361 KIHRRMDHYAAETRQDKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
QY 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
QY 481 LPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
Db 481 LPKRLHYANNRRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
QY 541 VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLRTNTRPTMPEEV 600
```


QY 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLRYT 660
Db 549 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLRYT 608
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCL 720
Db 609 RYDILYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCL 668
QY 721 AYKNDKQMSYGFLFPPYLSSSPKAYDAFLVTNMVPMYPAFKRVWNYFQRLVVKKYASER 780
Db 669 AYKNDKQMSYGFLFPPYLSSSPKAYDAFLVTNMVPMYPAFKRVWNYFQRLVVKKYASER 728
QY 781 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
Db 729 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900
Db 789 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 848
QY 901 ILTLKTYLHTYESEI 915
Db 849 ILTLKTYLHTYESEI 863
RESULT 3
Q15117 PRELIMINARY; PRT; 863 AA.
AC Q15117;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
RL Genomics 30:380-384(1995).
DR EMBL; D45421; BAA08260.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99040 MW; 318EA28B1CEA7A55 CRC64;

Query Match 93.0%; Score 4666; DB 4; Length 863;
Best Local Similarity 93.4%; Pred. NO. 0;
Matches 855; Conservative 3; Mismatches 5; Indels 52; Gaps 1;

QY 1 MARRSSFQSCQIIISLFFAVGVSIICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60
Db 1 MARRSSFQSCQIIISLFFAVGVNICLGFTAHRIKRAEGWEEGPTVLSDSPWTNIGSCK 60
QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
Db 61 GRCFELQEAGPPCHRCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHWVDDCEEIKAAECGAGFVRPPLIIFSVDGFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHWVDDCEEIKAAECGAGFVRPPLIIFSVDGFRASYMK 180

QY 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSKVMPIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERRILITLRLWLTLPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSVIPHERRILITLRLWLTLPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGFPGPEESSYSGSPFPAKRPKRKVAPKRQRPVAPPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGFPGPE----- 324
QY 361 KIHRLMDHYAAETRDQKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVDHGMEDVTCD 420
Db 325 -----MTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVDHGMEDVTCD 368
QY 421 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPAKAIANLTCKKPDQHFKPYLKQH 480
Db 369 RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPAKAIANLTCKKPDQHFKPYLKQH 428
QY 481 LPKRLHYANNRRIEDIHLVERRRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 540
Db 429 LPKRLHYANNRRIEDIHLVERRRWHVARKPLDVYKKPSGKCFQGDHGFNDKVNMQTVF 488
QY 541 VGYGPTFKYKTKVPPFENIELYNMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 600
Db 489 VGYGPTFKYKTKVPPFENIELYNMCDLLGLKPAPNNGTHGSLNHLRLTNTFRPTMPEEV 548
QY 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLRYT 660
Db 549 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGSTEERHLLYGRPAVLRYT 608
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCL 720
Db 609 RYDILYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSRVPDHLTSCVRPDVVRVSPFSQNCL 668
QY 721 AYKNDKQMSYGFLFPPYLSSSPKAYDAFLVTNMVPMYPAFKRVWNYFQRLVVKKYASER 780
Db 669 AYKNDKQMSYGFLFPPYLSSSPKAYDAFLVTNMVPMYPAFKRVWNYFQRLVVKKYASER 728
QY 781 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
Db 729 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900
Db 789 LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 848
QY 901 ILTLKTYLHTYESEI 915
Db 849 ILTLKTYLHTYESEI 863
RESULT 4
Q9R1E6 PRELIMINARY; PRT; 862 AA.
AC Q9R1E6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).
GN NPPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B/6;
RA Sano K., Piao J.-H.;
RT "Cloning and chromosomal assignment of mouse phosphodiesterase
RT I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";


```
Db 322 -----MTNPLREIDKTVGQMDGLKQLRLHRCVNVIFVGDHG 358
QY 414 MEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHF 473
Db 359 MEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRAKSINNSKYDPKTIIANLTCKKPDQHF 418
QY 474 KPYLKQHLPKRLHYANNRRIEDIHLVVERKWHVARKPLDVYKKPSGKCFQGDHGFKNV 533
Db 419 KPYMKQHLPKRLHYANNRRIEDIHLVDRWHVARKPLDVYKKPSGKCFQGDHGFKNV 478
QY 534 NSMQTVFVGYPTEFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTFR 593
Db 479 NSMQTVFVGYPTEFKYKTKVPPFENIELYNVMDLLGLKPAPNNGTHGSLNHLRTNTFR 538
QY 594 PTMPEEVRPNYPGIMYLSQDFDLGCTCDKVEPKNKLDLNLKRLHTKGTGTE----- 645
Db 539 PTMPDEVSRPNYPGIMYLSQSEFDLGCTCDKVEPKNKLEELNKRHLTKGTGTEAETGKFRG 598
QY 646 -----ERHLLYGRPAVLRYTRYDILYHTDFESGYSEIFLMLLWTSYTV 688
Db 599 SKHENKKNLNGSVEPRKERHLLYGRPAVLRYTSYDILYHTDFESGYSEIFLMLLWTSYTI 658
QY 689 SKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCLAYKNDQMSYGFLLPFPYLSSSSPEAKYDA 748
Db 659 SKQAEVSSIPEHLTNCVRPDVVRVSPGFSQNCLAYKNDQMSYGFLLPFPYLSSSSPEAKYDA 718
QY 749 FLVTNMVPMYPAFKRVWNYFORVLVKYASERNGVNIVSGPIFDYDYGDLHDTEDKIKQY 808
Db 719 FLVTNMVPMYPAFKRVWAYFORVLVKYASERNGVNIVSGPIFDYDYGDLRDEIDEIKQY 778
QY 809 VEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWV 868
Db 779 VEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWV 838
QY 869 EELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKYLHTYSEI 915
Db 839 EELMKMHTARVRDIEHLTGLDFYRKTSRSYSEILTLTKYLHTYSEI 885

RESULT 6
Q63490
ID Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RB13-6 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=95247775; PubMed=7730366;
RA Deissler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
RT and tumor cell surface antigen gpl30RB13-6 reveals relationship to
RT human and murine PC-1."
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL; Z47987; CAA88029.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 9BA9FBFEF82DFBA6 CRC64;
```

Query Match

41.5%; Score 2084; DB 11; Length 875;

```
Best Local Similarity 43.5%; Pred. No. 9.6e-162;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;
QY 57 GSCKGRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116
Db 53 GSCRKKCFDSSHRGLEGRCDSDGCTDRGDCWDFEDTCVKSTQIWTCSNFRGETRLEAA 112
QY 117 ACHCEDCLARGDCCTNYQVVCKGSHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRA 176
Db 113 LCSCADDCLQRKDCCTDYKAVCQGEVPPVWTEACASSQEQCEGDFQPPVILFSMDGFRA 172
QY 177 SYMKGSKVMPNIEKLRSCGTHSPMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP 236
Db 173 EYLQWTSTLLPNINKLKTGCLHSHKYMAMYPTKTFPNHYTIVTGLYPESHGIIDNNMYDV 232
QY 237 VEDATFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SV 278
Db 233 YLNKNFSLSSVEKSNPAWWSGQFIWLTAMYQGLKAAASYWLGSDVAVNGSFPNIYRYSN 292
QY 279 VIPHERRILTLRWLTLPDHERPSVYAFYSEQPDFSGHKYGFPGPEESSYGSPTPAKRP 338
Db 293 SVPYESRIATLLQWLDLPKAERPSTYTIYVEEPSAGHKSPV-----SAG----- 338
QY 339 KRKVAPKRRQERPVPAPPKRRRKIRHMDHYAAETRQDKMTNPREIDKIVGQMDGLKQL 398
Db 339 -----VIKALQLVDDAFGLMEGLKQR 360
QY 399 KLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDQTSRDRVEYMTDYFPEI-NFYMYQGAPAPRITRNIPQDFFTFN 419
QY 453 AKYDPKAIIANLTCKKPDQHFEPYLPKQHLPKRLHYANNRRIEDIHLVERRWHVARKPLD 512
Db 420 S-----EEIVRDLSCRKSDQHFAPYLTPLDLPKRLHYAKNVRIDKVLHVMVDRQWLAYR---- 471
QY 513 VYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGPTFKYKTKVPPFENIELYNVMDLLGLK 572
Db 472 --NKGSSNC-EGGTHGYNNEPKSMEAIFLAHGPSFKEKTVIEPFENIEVYNLLCDLLHIQ 528
QY 573 PAPNNGTHGSLNHLRTNFRPTMPEEVRPNYPGIMYLSQDFDLGCTCDKVEPKNKLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQPSHAEELSKSAGCGFTTPLPKDSLNCSC-LALQTSQEE 587
QY 633 ELNKRHLTKG---STEERHLLYGRPAVLRYTR-YDILYHTDFESGYSEIFLMLLWTSYT 687
Db 588 QVNQRNLNSGGEVSATEKTNLPFGRPRVIOKNKDCHLLYHREYVSGFGKAMKMPMWSST 647
QY 688 VSKQAEVSSVPDHLTSCVRPDVVRVSPFSQNCLAYKNDQMSYGFLLPFPYLSSSSPEAKYD 747
Db 648 VPKPGDTSSLPPTVPDCLRADVRVDPSESKCSFYLADQNIDHGLFYPPIAIGNNESQYD 707
QY 748 AFLVTNMVPMYPAFKRVWNYFORVLVKYASERNGVNIVSGPIFDYDYGDLHDTEDKIKQ 807
Db 708 ALITSNLVPMYKEFKKMWDFHKVLLIKYAIERNGVNVVSGPIFDYDYGDLHDTEDKIKQ 767
QY 808 YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKW 867
Db 768 YVAGTDVPVPTHYFVVLTSCKNKTHTPDSCPGWLDVLPFVVPVHRPTNVESCPENKAEDLW 827
QY 868 VEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKYLHTYSEI 915
Db 828 VEERFKAHIAVRDVELLTGLDFYQEKTPQVSEILQLTKYLPFTETII 875

RESULT 7
P97676
ID P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
```


Db 339 -----VIKALQLVDDAFGLMEGLKQR 360

QY 399 KLRRCVNVIFVDHGMEDVTCDRTEFLSNLTVNDDITLVPGLGRIRSK-----FSNN 452

Db 361 NLHNCVNIIVLADHGMQDTSQDRVEYMTDYFPEI-NFYMYQGPAPIRTRNIPQDFFTFN 419

QY 453 AKYDPKAIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLD 512

Db 420 S-----EIVRDLSCRKSDQHFKPYLTPDLPKRLHYAKNVRIDKVHLMVDRLQWLAYR---- 471

QY 513 VYKKPSGCKFFQGDHGFNDKVNMSQTVFVGYPTEFKYKTKVPPPFENIELYNVCMDDLGLK 572

Db 472 --NKGSSNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVEIEPFENIEVYNLLCDLLHIQ 528

QY 573 PAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLD 632

Db 529 PAPNNGSHGSLNHLKAPFYQPSHAEELSKSAGCGFTTLPKDSLNCSC-LALQTSQEE 587

QY 633 ELNKRHLTK-----GSTEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687

Db 588 QVNQRLNLRGEVSATEKTNLPFGRPRVIOKNKDHCLLYHREYVSGFGKAMKMPMWSSYT 647

QY 688 VSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPYLSSSPEAKYD 747

Db 648 VPKPGDTSSLPTVPDCLRADVRVDPSESQKCSFYLADQNIDHGFLYPPPAIKGNESQYD 707

QY 748 AFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIKQ 807

Db 708 ALITSNLVPMYKEFKKMWDYFHVKVLLIKYAIERNGVNVISGPIFDYDGHFDAPDEITN 767

QY 808 YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPNDEESNSEDSESKW 867

Db 768 YVAGTDVPVPTHYFVWLTSCKNKTHTPDSCPGWLDVLPFVVPHRPTNVESCPENKAEDLW 827

QY 868 VEELMKMHTARVRDIEHLTSLDFFRKTSSYPEILTKTYLHTYESEI 915

Db 828 VEERFKAHIAVRDVELLTGLDFYQEKTPQVSEILQLKTYLPTFETII 875

RESULT 9

P70641

ID P70641 PRELIMINARY; PRT; 876 AA.

AC P70641;

DT 01-FEB-1997 (TremBLrel. 02, Created)

DT 01-FEB-1997 (TremBLrel. 02, Last sequence update)

DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)

DE PHOSPHODIESTERASE I.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;

RA Sano K.;

RT "Molecular cloning of phosphodiesterase I cDNA from rat small intestine."

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; D30649; BAA06333.1; -.

DR InterPro; IPR001212; -.

DR InterPro; IPR001604; -.

DR InterPro; IPR002591; -.

DR Pfam; PF01033; Somatomedin_B; 2.

DR Pfam; PF01663; Phosphodiester; 1.

DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.

DR SMART; SM00477; NUC; 1.

SQ SEQUENCE 876 AA; 99328 MW; D2F772C34A0C437A CRC64;

Query Match 41.0%; Score 2057.5; DB 11; Length 876;
Best Local Similarity 43.2%; Pred. No. 1.4e-159;
Matches 384; Conservative 159; Mismatches 251; Indels 95; Gaps 12;

QY 57 GSKGRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116

Db 53 GSKRKKCFDSSHRGLEGRCDSDGTDRCDCWDFEDTCVKSQIWTCSNFCGETRLETA 112

QY 117 ACHSEDCLARGDCCTNYQVCKGESHVWDDCEEIKAAECFAGFVRPPLIIFSVDGFRA 176

Db 113 LSCADDDCLQRKDCCTDYKAVCGEVPWVTEACASSQEQPCGEGDQPPVILFSMDGFRA 172

QY 177 SYMKGSKVMPNIEKLRSCTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP 236

Db 173 EYLQWSTLLPNINKLTKCGLHSKYMRVYPTKTFPNHYTIVTGLYPESHGIIDNNMYDV 232

QY 237 VFDATFHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SV 278

Db 233 YLNKNFSLSSVEKSNPAWWSGQIWLTAHYQGLKAASYWPBGSDVAVNGSFPNIYRYSN 292

QY 279 VIPHERRILTLRWLTLPDHERPSYAFYSEQPDFSGHKYGFPGPEESSYGSPTPAKRP 338

Db 293 SVPEYESRIATLLQWLDPKAERPSPYTIYVEEPDSAGHKSGPV-----SAG----- 338

QY 339 KRKVAPKRRQERPVPAPPKRRRKIRHMDHYAAETRODKMTNPLREIDKIVGQMLDGLKQL 398

Db 339 -----VIKALQLVDDAFGLMEGLKQR 360

QY 399 KLRRCVNVIFVDHGMEDVTCDRTEFLSNLTVNDDITLVPGLGRIRSK-----FSNN 452

Db 361 NLHNCVNIIVLADHGMQDTSQDRVEYMTDYFPEI-NFYMYQGPAPIRTRNIPQDFFTFN 419

QY 453 AKYDPKAIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRRIEDIHLLVERRWHVARKPLD 512

Db 420 S-----EIVRDLSCRKSDQHFKPYLTPDLPKRLHYAKNVRIDKVHLMVDRLQWLAYR---- 471

QY 513 VYKKPSGCKFFQGDHGFNDKVNMSQTVFVGYPTEFKYKTKVPPPFENIELYNVCMDDLGLK 572

Db 472 --NKGVPNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVEIEPFENIEVYNLLCDLLHIQ 528

QY 573 PAPNNGTHGSLNHLRLTNTFRPTMPEEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLD 632

Db 529 PAPNNGSHGSLNHLKAPFYQPSHAEELSKSAGCGFTTLPKDSLNCSC-LALQTSQEE 587

QY 633 ELNKRHLTK-----GSTEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687

Db 588 QVNQRLNLRGEVSATEKTNLPFGRPRVIOKNKDHCLLYHREYVSGFGKAMKMPMWSSYT 647

QY 688 VSKQAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSYGFLEPPYLSSSPEAKYD 747

Db 648 VPKPGDTSSLPTVPDCLRADVRVDPSESQKCSFYLADQNIDHGFLYPPPAIKGNESQYD 707

QY 748 AFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIKQ 807

Db 708 ALITSNLVPMYKEFKKMWDYFHVKVLLIKYAIERNGVNVISGPIFDYDGHFDAPDEITN 767

QY 808 YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPNDE-ESCNSEDSESK 866

Db 768 YVAGTDVPVPTHYFVWLTSCKNKTHTPDSCPGWLDVLPFVVPHRPTKPVESCPENKAEDL 827

QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSSYPEILTKTYLHTYESEI 915

Db 828 WVEERFKAHIAVRDVELLTGLDFYQEKTPQVSEILQLKTYLPTFETII 876

RESULT 10

O14638

ID O14638 PRELIMINARY; PRT; 875 AA.

AC O14638;

DT 01-JAN-1998 (TremBLrel. 05, Created)

DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)

DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)

DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)

DE (PHOSPHODIESTERASE I BETA).

GN PDNP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 27 SCKGRCFE-RTFG--NCRCDAAACVELGNCCLDYQETCIEPEHIWTCNKRFCGEKRLTRSL 83

QY 118 CHCSEDCIARGDCCTNYQVVCKGESHVDDCEEIKAAECFAGFVRPPLIIFSVDFGRAS 177

Db 84 CACSDCKDKGDCCCINYSVQCQGEKSWVEEPCESINEPQCPAGFETPTPLFLSLDGFRAE 143

QY 178 YMKKGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237

Db 144 YLHTWGLLPVISKLLKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGIIDNKMYPDK 203

QY 238 FDATEHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SVV 279

Db 204 MNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWPGSDVEINGIFPDIYKMYNGS 263

QY 280 IPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSFPTPAKRPK 339

Db 264 VPFEERILAVLQWLQPKDERPHFYTLYLEEPDSSGHSYGPVSSE----- 308

QY 340 RKVAPKRRQERPVPAPPKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQGLMDGLKQLK 399

Db 309 -----VIKALQRVDGMVGMMLDGLKELN 331

QY 400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTGLGRIR-----SKFSNNAK 454

Db 332 LHRCLNLILISDHGMEQGSCKKYIYLNKYLGDVKNIKVIYGPAARLPSDVPDKYYS--- 388

QY 455 YDPKAIILANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLDVI 514

Db 389 FNYEGIARNLSCREPNOHFEPYKHLFHPKRLHFAKSDRIEPLTFYLDPOWQALNPSE-- 446

QY 515 KKP SGKCFQGDHGFNDKNVSMQVVFVGYGPTFKYKTKVPPFENIELYNVCMDDLGLKPA 574

Db 447 RKYCG---SGFHGSDNVFSNMQALFVGYGPGFKHGIEADTFENIEVYNLMDLLNLTPA 502

QY 575 PNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMYLSQDF-----DLGCTCDDKVEPK 628

Db 503 PNNGTHGSLNHLKPNVYTPKHPRV---HP---LVQCPFTRNPRDNLGCSCNPILP- 554

QY 629 NKLDELNKRHLTKGSTEE--RH--LLYGRPAVLYR-TRYDILYHTDFESGYSEIFLMLLW 683

Db 555 --IEDFQTFNLTVAAEEKIHKHETLPYGRPRVLQKENTICLLSQHQFMSGYSQDILMPLW 612

QY 684 TSYTVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCLAYKNDKQMSYGFLEPPYLSSSPE 743

Db 613 TSYTVDRNDSFST--EDFSNCLYQDFRIPLSPVHKCSFYKNNTKVSYGELSPQLNKNSS 670

QY 744 AKY-DAFLVTNMVMPYPAFKRVWNYFQRLVKKYASERNGVNVISGPIDFYDYDGLHDE 802

Db 671 GIYSEALLTNIIVPMYQSFQVIWRYFHDTLRLKYAEERNGVNVVSGPVDFDYDGRCDL 730

QY 803 DKIKQ---YVEGSSIPVPTHYSITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESC 859

Db 731 ENLRQKRRVIRNQEILIPTHFFIVLTSCKDTSTQPLHCEN-LDTLAFILPHRTDNSESCV 789

QY 860 SSEDESKWVEELMKMHTARVDIEHLTSLDFFRKTSRYSYPEILTLKTYLHTYESE 914

Db 790 HGKHDSSWVEELMLHARITDVEHITGLSFYQQRKEPVSDILKTLHLPTFSQE 844

RESULT 12

Q9P1P6 PRELIMINARY; PRT; 925 AA.

AC Q9P1P6;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

DE PDNP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Bozzali M., Pizzuti A., Trischitta E.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AF110304; AAF36094.1; -

DR EMBL; AF110280; AAF36094.1; JOINED.

DR EMBL; AF110281; AAF36094.1; JOINED.

DR EMBL; AF110283; AAF36094.1; JOINED.

DR EMBL; AF110284; AAF36094.1; JOINED.

DR EMBL; AF110285; AAF36094.1; JOINED.

DR EMBL; AF110286; AAF36094.1; JOINED.

DR EMBL; AF110287; AAF36094.1; JOINED.

DR EMBL; AF110288; AAF36094.1; JOINED.

DR EMBL; AF110289; AAF36094.1; JOINED.

DR EMBL; AF110290; AAF36094.1; JOINED.

DR EMBL; AF110291; AAF36094.1; JOINED.

DR EMBL; AF110292; AAF36094.1; JOINED.

DR EMBL; AF110293; AAF36094.1; JOINED.

DR EMBL; AF110294; AAF36094.1; JOINED.

DR EMBL; AF110295; AAF36094.1; JOINED.

DR EMBL; AF110296; AAF36094.1; JOINED.

DR EMBL; AF110297; AAF36094.1; JOINED.

DR EMBL; AF110298; AAF36094.1; JOINED.

DR EMBL; AF110300; AAF36094.1; JOINED.

DR EMBL; AF110301; AAF36094.1; JOINED.

DR EMBL; AF110302; AAF36094.1; JOINED.

DR EMBL; AF110303; AAF36094.1; JOINED.

DR InterPro; IPR001212; -

DR InterPro; IPR001604; -

DR InterPro; IPR002591; -

DR Pfam; PF01033; Somatomedin_B; 2.

DR Pfam; PF01663; Phosphodiester; 1.

DR PRINTS; PR00022; SOMATOMEDINB.

DR PROSITE; PS00524; SOMATOMEDIN_B; 2.

DR SMART; SM00477; NUC; 1.

SQ SEQUENCE 925 AA; 104924 MW; 0ECAA063801CAFEBCRC64;

Query Match 39.0%; Score 1955.5; DB 4; Length 925;

Best Local Similarity 42.2%; Pred. No. 3.4e-151;

Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19;

QY 58 SCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENA 117

Db 107 SCKGRCFE-RTFG--NCRCDAAACVELGNCCLDYQETCIEPEHIWTCNKRFCGEKRLTRSL 163

QY 118 CHCSEDCIARGDCCTNYQVVCKGESHVDDCEEIKAAECFAGFVRPPLIIFSVDFGRAS 177

Db 164 CACSDCKDKGDCCCINYSVQCQGEKSWVEEPCESINEPQCPAGFETPTPLFLSLDGFRAE 223

QY 178 YMKKGSKVMNPNIKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237

Db 224 YLHTWGLLPVISKLLKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGIIDNKMYPDK 283

QY 238 FDATEHLRGREKFNHRWGGQPLWITATKQGVKAGTFFW-----SVV 279

Db 284 MNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWPGSDVEINGIFPDIYKMYNGS 343

QY 280 IPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSFPTPAKRPK 339

Db 344 VPFEERILAVLQWLQPKDERPHFYTLYLEEPDSSGHSYGPVSSE----- 388

QY 340 RKVAPKRRQERPVPAPPKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQGLMDGLKQLK 399

Db 389 -----VIKALQRVDGMVGMMLDGLKELN 411

QY 400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTGLGRIR-----SKFSNNAK 454

Db 412 LHRCLNLILISDHGMEQGSCKKYIYLNKYLGDVKNIKVIYGPAARLPSDVPDKYYS--- 468

QY 455 YDPKAIILANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLDVI 514

Db 469 FNYEGIARNLSCREPNOHFEPYKHLFHPKRLHFAKSDRIEPLTFYLDPOWQALNPSE-- 526

QY	515	KKPSGKCFQGDHGFNDKVN	574
Db	527	RKYCG---SGFHGSDNVFS	582
QY	575	PNNGTHGSLNHLRLTNT	628
Db	583	PNNGTHGSLNHLKPNVY	634
QY	629	NKLDELNKRHLTKGSTEE	683
Db	635	--IEDFQTQFNLTVAEEK	692
QY	684	TSYTVSKQAEVSSVPDHL	743
Db	693	TSYTVDRNDSFST--EDF	750
QY	744	AKY-DAFLVTNMVPMYP	802
Db	751	GIYSEALLTNIIVPMYQ	810
QY	803	DKIKQ---YVEGSSIPV	859
Db	811	ENLRQKRRVRIRNQEIL	869
QY	860	SSEDESKWVEELMKMHT	914
Db	870	HGKHDSSWVEELMLHR	924
RESULT 13			
O90761	PRELIMINARY; PRT; 817 AA.		
ID	O90761		
AC	O90761;		
DT	01-NOV-1998 (TremBLrel. 08, Created)		
DT	01-NOV-1998 (TremBLrel. 08, Last sequence update)		
DT	01-MAR-2001 (TremBLrel. 16, Last annotation update)		
DE	ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-		
DE	NUCLEOTIDE PHOSPHODIESTERASE).		
GN	PC1.		
OS	Fowlpox virus.		
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
OC	Avipoxvirus.		
OX	NCBI_TaxID=10261;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FP-9;		
RX	MEDLINE=98325194; PubMed=9658122;		
RA	Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;		
RT	"Fowlpox virus encodes nonessential homologs of cellular alpha-SNAP,		
RT	PC-1, and an orphan human homolog of a secreted nematode protein."		
RL	J. Virol. 72:6742-6751(1998).		
CC	-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES		
CC	SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED		
CC	OLIGO-NUCLEOTIDES.		
DR	EMBL; AJ006408; CAA07014.1; -.		
DR	InterPro; IPR001604; -.		
DR	InterPro; IPR002591; -.		
DR	Pfam; PF01663; Phosphodiesterase; 1.		
DR	SMART; SM00477; NUC; 1.		
KW	Hydrolase.		
SQ	SEQUENCE 817 AA; 94004 MW; CB68DA0508CC568E CRC64;		
Query Match 22.9%; Score 1151; DB 14; Length 817;			
Best Local Similarity 32.4%; Pred. No. 1.9e-85;			
Matches 263; Conservative 141; Mismatches 276; Indels 132; Gaps 21;			
Qy	131	CTNYQVCKGESHVDDDC	190
Db	104	CISFQVT-----CPPE	144
Qy	191	KLRSCGTHSPYMRPVY	250

Db	145	DLMEHGVTAAP-MRPVYPTNTFPNLYSIVTGLYPISHGITDNEFIDRGTDIEFTIASEETE	203
QY	251	NHRWGGQPLWITATKQGVKAGTFEW---SVV-----IPHERRLITLRW	292
Db	204	EVENFGGEPITWTIMKNGFKSATFFWPGSDKVVPKRPTMYRSYNSKVPYEEINTVLRW	263
QY	293	LTLPDHERPSVYAFYSEQPDFSGHKYGFPGPEESSYGSPTTAPKRPKRVAPKRRQRPV	352
Db	264	LKMDTYRPFYFALYLEEPGSSGYEYG-----	290
QY	353	APPKRRRKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH	412
Db	291	-----TDDERVGKALEKVDKAIALLMKGLKDLQLIGCANLILVSDH	331
QY	413	GMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAK-YDPKAIIANLTCKKPDQ	471
Db	332	GMSNVDPKKIVNLKDYITN-NDVVIKPGATPVIKPQNLNHIRLFDYDGIISSTSCVMDDQ	390
QY	472	HFKPYLKQHLPKRLHYANNRRIEDIHLVERRWHVARKPLDVYKKPSGCKCFEQGDHGFN	531
Db	391	PFIVSYRSRLPKRLHYSGGFRTEILGVYLEEGWQSTDENGL-KHRSG----GFHGSND	444
QY	532	KVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLGLKPAPNNGTHGSLNHLRLTNT	591
Db	445	SFQDMTAVFLGYGPAFLDDVRVPIDFNIELYNMMCEILGINPANNGTVGSLNNILNSR	504
QY	592	FRP-----TMPEEVTRPNYPGIMYLSQSDFDLGCTCD--DKVEPKNKDELNKLHTKG	642
Db	505	YTHVSSLDIITIESECDRHAYVG-----DHLKGCTCKNIDRFSSKGNKEDSSR---TRS	555
QY	643	STEERHLLYGRPAVLRY-RTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHL	701
Db	556	SSYIYNLPFGKPAVLLNRHHHCIIKNDNVVTAYSKVNRLPLWTSFSI--DITYNSTNIYN	613
QY	702	TSCVRPDVRVSPFSQNCLAYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAF	761
Db	614	KTCYLQDMRVM-YYPEPCRYYSTQKDVYGYLYP----ARATDFQSLLTETNTPVPMYRNF	667
QY	762	KRVWNYFQRLVKKYASERNGVNVISGPIFDYDYGDLHDTEDKIKQ---YVEGSSIPVPT	818
Db	668	KKIWEVFMSSILIEYVQKHVVNVVMVGPVFDNSNGIRDSDWLISMSSGY--NNKVYIPS	725
QY	819	HYYSIITSCLDFTQPADKCDGLSVSSFILPHRPD-NEESCNSSEDES-KWVEELMKMHT	876
Db	726	DYFVILTYCKDKDSSLNDCYSNIKTESFVVPNSDTYYNESCSRENITSVSVVRKIFSLHR	785
QY	877	ARVRDIEHLTSLDFFRKTSRSYPEILTLKTYL 908	
Db	786	VRIKDIETVTSMSFYRNRYKTSNNVAVLKTVM 817	
RESULT 14			
O9J5H1	PRELIMINARY; PRT; 817 AA.		
ID	O9J5H1		
AC	O9J5H1;		
DT	01-OCT-2000 (TremBLrel. 15, Created)		
DT	01-OCT-2000 (TremBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TremBLrel. 16, Last annotation update)		
DE	ORF FPV030 ALKALINE PHOSPHODIESTERASE.		
GN	FPV030.		
OS	Fowlpox virus.		
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
OC	Avipoxvirus.		
OX	NCBI_TaxID=10261;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20193820; PubMed=10729156;		
RA	Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;		
RT	"The genome of fowlpox virus."		
RL	J. Virol. 74:3815-3831(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;		

Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL	EMBL; AF198100; AAF44374.1; -.
DR	InterPro; IPR001428; -.
DR	InterPro; IPR001604; -.
DR	InterPro; IPR002591; -.
DR	InterPro; IPR003232; -.
DR	Pfam; PF01663; Phosphodiester; 1.
DR	ProDom; PD000946; -; 1.
DR	ProDom; PD004900; -; 1.
DR	SMART; SM00477; NUC; 1.
SQ	SEQUENCE 817 AA; 94038 MW; 8404FD00641DA022 CRC64;

```

RESULT 15
Q9SU82
AC Q9SU82; PRELIMINARY; PRT; 457 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE NUCLEOTIDE PYROPHOSPHATASE-LIKE PROTEIN (EC 3.6.1.9).
GN T16L4.200 OR AT4G29690.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.
RL Submitted (MAR-2000) to the EMBL/GenBank/DBBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AL079344; CAB45329.1; -
DR EMBL; AL161575; CAB79727.1; -
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hydrolase.
SQ SEQUENCE 457 AA; 51261 MW; 3B95E6C0AE1B1215 CRC64;

```


Db 388 GYDNMFFSMRSIFVGYGPRFRGKVPSEFENVQYNAVAEILGLRPAPNNGS 439

Search completed: July 19, 2001, 14:46:48
Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:00 ; Search time 34.65 Seconds
(without alignments)
22.745 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	22	AA1992
2	76	100.0	788	17	AA198579
3	76	100.0	829	17	AA198578
4	76	100.0	858	22	AA19986
5	76	100.0	858	22	AA19995
6	76	100.0	858	22	AA19996
7	76	100.0	858	22	AA19997
8	76	100.0	858	22	AA19998
9	76	100.0	858	22	AA19999
10	76	100.0	859	22	AA19991
11	76	100.0	863	22	AA19988
					Autotaxin phosphod
					Autotaxin derived
					Autotaxin derived
					Rat autotaxin prot
					Rat autotaxin vari
					Rat autotaxin vari
					Rat autotaxin vari
					Rat autotaxin vari
					Human autotaxin pr
					Human teratocarcin

12	76	100.0	915	17	AA198596	A2058 autotaxin pr
13	76	100.0	915	22	AA198579	Human melanoma aut
14	76	100.0	979	17	AA198580	Autotaxin derived
15	71	93.4	849	17	AA198595	N-tera 2D1 autotax
16	70	92.1	885	22	AA198599	Rat brain autotaxi
17	69	90.8	873	21	AA1983620	Human PC-1 polypep
18	69	90.8	873	21	AA1983621	Variant human PC-1
19	69	90.8	925	16	AA198148	Human insulin rece
20	69	90.8	925	20	AA198355	Insulin receptor t
21	69	90.8	925	21	AA1980195	Breast cancer prot
22	49	64.5	400	21	AA1982975	Arabidopsis thalia
23	49	64.5	457	21	AA1981321	Arabidopsis thalia
24	49	64.5	461	21	AA1982974	Arabidopsis thalia
25	49	64.5	465	21	AA1982973	Arabidopsis thalia
26	43	56.6	173	20	AA1980784	Renal cancer assoc
27	43	56.6	263	18	AA19840374	Human breast cance
28	43	56.6	263	18	AA19801573	Protein encoded by
29	43	56.6	263	21	AA1984037	Amino acid sequenc
30	43	56.6	562	21	AA1983329	Human colon cancer
31	43	56.6	579	18	AA19840378	Human breast cance
32	43	56.6	579	21	AA1984041	Amino acid sequenc
33	42	55.3	411	20	AA19834445	Porphyromonas ging
34	42	55.3	428	20	AA19834324	Porphyromonas ging
35	42	55.3	528	22	AA19879259	Corynebacterium gl
36	42	55.3	530	22	AA19879258	Corynebacterium gl
37	41	53.9	109	19	AA19852839	Secreted protein e
38	41	53.9	453	20	AA19817529	Human secreted pro
39	41	53.9	453	20	AA19802378	Polypeptide identi
40	41	53.9	453	22	AA19890545	Human secreted pro
41	40	52.6	199	21	AA19844375	Arabidopsis thalia
42	40	52.6	199	21	AA1983821	Arabidopsis thalia
43	40	52.6	199	22	AA19868971	Sheep mitosis arre
44	40	52.6	199	22	AA19868972	Human mitosis arre
45	40	52.6	205	18	AA19813020	Human MAD2 protein

ALIGNMENTS

RESULT 1
AA1981992
ID AA1981992 standard; peptide; 13 AA.
XX
AC AA1981992;
XX
DT 28-MAR-2001 (first entry)
XX
DE Autotaxin phosphodiesterase catalytic site.
KW Autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity;
KW phosphodiesterase catalytic site.

OS Unidentified.

XX
PN WO200068386-A1.

XX
PD 16-NOV-2000.

XX
PF 05-MAY-2000; 2000WO-US12402.

XX
PR 07-MAY-1999; 99US-0306979.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Kelly JD;

XX
DR WPI; 2001-007397/01.

XX

PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
PS Disclosure; Page 3; 126pp; English.
XX
CC The present sequence is autotaxin phosphodiesterase catalytic
CC site. Phosphorylation of threonine residue at position 10 of this
CC sequence is required for autotaxin to undergo autophosphorylation
CC and exhibit phosphodiesterase and motility-stimulating activities.
CC Autotaxin is a glycoprotein cytokine which increases
CC insulin signalling in adipose tissue by producing substrate for
CC adenosine receptors, resulting in inhibition of lipolysis, and
CC decreased hepatic gluconeogenesis and serum glucose levels, and
CC increased insulin sensitivity. It also inhibits differentiation
CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
CC Autotaxin and its analogues are used to stimulate glucose uptake
CC by cells, particularly to reduce serum glucose levels for
CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 76; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 1 ymrpvpyptktfnp 13

RESULT 2
AAR86579
ID AAR86579 standard; Protein; 788 AA.
XX
AC AAR86579;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin derived from teratocarcinoma N-tera 2D1 cells.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9532221-A2.
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US06613.
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Krutzch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX
DR WPI; 1996-020533/02.
DR N-PSDB; AAT06613.
XX
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
PT
XX Claim 4; Page 62-65; 112pp; English.
PS
XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is

CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of AXT, while
CC having little effect on the membrane form of AXT.
XX
SQ Sequence 788 AA;

Query Match 100.0%; Score 76; DB 17; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 126 ymrpvpyptktfnp 138

RESULT 3
AAR86578
ID AAR86578 standard; Protein; 829 AA.
XX
AC AAR86578;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin derived from melanoma cell line A2058.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9532221-A2.
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US06613.
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Krutzch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX
DR WPI; 1996-020533/02.
DR N-PSDB; TO6612.
XX
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
PT
XX Claim 4; Page 57-60; 112pp; English.
PS
XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of AXT, while


```
CC having little effect on the membrane form of AXT.
XX
SQ Sequence 829 AA;

Query Match 100.0%; Score 76; DB 17; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 115 ymrpvpyptktfpn 127

RESULT 4
AAY71986
ID AAY71986 standard; Protein; 858 AA.
XX
AC AAY71986;
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin protein.
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Domain 5..15
FT /note= "Putative transmembrane domain"
FT Binding-site 122..124
FT /label= RGD_binding_domain
FT Region 143..158
FT /label= Epitope
FT /note= "This region is specifically claimed in claim 10"
FT Region 149..158
FT /label= Epitope
FT /note= "This region is specifically claimed in claim 10;
FT This region is absent in rat brain autotaxin designated
FT as PD-1alpha sequence (AAY71989)"
FT Active-site 196..208
FT /note= "Autotaxin phosphodiesterase catalytic site"
FT Region 585..595
FT /label= Epitope
FT /note= "This region is specifically claimed in claim 10"
FT
XX WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
DR N-PSDB; AAD02131.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Claim 1; Page 101-104; 126pp; English.
XX
CC The present sequence is rat autotaxin protein. Autotaxin is a
```

```
CC glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic
CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 196 ymrpvpyptktfpn 208

RESULT 5
AAY71995
ID AAY71995 standard; Protein; 858 AA.
XX
AC AAY71995;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (A93V).
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 93
FT /note= "Wild type Ala substituted by val"
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Disclosure; Page -; 126pp; English.
XX
CC The present sequence is variant (A93V) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic
```

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 196 ymrpvpyptktfpn 208

RESULT 6
AAY71996
ID AAY71996 standard; Protein; 858 AA.
XX
AC AAY71996;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (A194V).
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Ala substituted by Val"
FT
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Disclosure; Page -; 126pp; English.
XX
CC The present sequence is variant (A194V) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 196 ymrpvpyptktfpn 208

RESULT 7
AAY71997
ID AAY71997 standard; Protein; 858 AA.
XX
AC AAY71997;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (S236T).
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 236 /note= "Wild type Ser substituted by Thr"
FT
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Disclosure; Page -; 126pp; English.
XX
CC The present sequence is variant (S236T) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 196 ymrpvpyptktpn 208

RESULT 8
AAY71998
ID AAY71998 standard; Protein; 858 AA.
XX
AC AAY71998;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (R265K).
XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
XX
OS Rattus sp.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 265 /note= "Wild type Arg substituted by Lys"
FT
XX

PN WO200068386-A1.

PD 16-NOV-2000..

PF 05-MAY-2000; 2000WO-US12402.

PR 07-MAY-1999; 99US-0306979.

PA (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

PI
XX
DR WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
XX Disclosure; Page -: 126pp; English.

XX The present sequence is variant (R265K) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 196 ymrpvpyptktpn 208

RESULT 9
AAY71999
ID AAY71999 standard; Protein; 858 AA.
XX
AC AAY71999;
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (S289T).
XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
XX
OS Rattus sp.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 289 /note= "Wild type Ser substituted by Thr"
FT
XX

PN WO200068386-A1.

PD 16-NOV-2000.

PF 05-MAY-2000; 2000WO-US12402.

PR 07-MAY-1999; 99US-0306979.

PA (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

PI
XX
DR WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
XX Disclosure; Page -: 126pp; English.

XX The present sequence is variant (S289T) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).

XX SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 196 ymrpvpyptktpn 208

RESULT 10
AAY71991

ID AAY71991 standard; Protein; 859 AA.

XX AC AAY71991;

XX DT 28-MAR-2001 (first entry)

XX DE Human autotaxin protein.

XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Domain 8..26
FT /note= "Putative transmembrane domain"
FT Cleavage-site 44..45
FT Binding-site 123..125
FT /label= RGD_binding_domain
FT Active-site 197..209
FT /note= "Putative phosphodiesterase active site"

XX PN WO200068386-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.
N-PSDB; AAD02133.

XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX Claim 27; Page 119-121; 126pp; English.

XX CC The present sequence is human autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases
CC insulin signalling in adipose tissue by producing substrate for
CC adenosine receptors, resulting in inhibition of lipolysis,
CC decreased hepatic gluconeogenesis and serum glucose levels, and
CC increased insulin sensitivity. It also inhibits differentiation
CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
CC Autotaxin and its analogues are used to stimulate glucose uptake
CC by cells, particularly to reduce serum glucose levels for
CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.

XX SQ Sequence 859 AA;

Query Match 100.0%; Score 76; DB 22; Length 859;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 197 ymrpvpyptktpn 209

RESULT 11
AAY71988

ID AAY71988 standard; Protein; 863 AA.

XX AC AAY71988;

XX DT 28-MAR-2001 (first entry)

XX DE Human teratocarcinoma autotaxin.

XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Binding-site 127..129
FT /label= RGD_binding_domain
FT Active-site 201..213
FT /note= "Autotaxin phosphodiesterase catalytic site"

XX PN WO200068386-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.

XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX Claim 27; Page 108-110; 126pp; English.

CC The present sequence is autotaxin isolated from human
CC teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which
CC increases insulin signalling in adipose tissue by producing substrate
CC for adenosine receptors, resulting in inhibition of lipolysis,
CC decreased hepatic gluconeogenesis and serum glucose levels, and
CC increased insulin sensitivity. It also inhibits differentiation
CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
CC Autotaxin and its analogues are used to stimulate glucose uptake
CC by cells, particularly to reduce serum glucose levels for
CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.
XX
SQ Sequence 863 AA;

Query Match 100.0%; Score 76; DB 22; Length 863;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 201 ymrpvpyptktfpn 213

RESULT 12
AAR86596
ID AAR86596 standard; Protein; 915 AA.
XX
AC AAR86596;
XX
DT 01-JUL-1996 (first entry)
XX
DE A2058 autotaxin protein.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
OS Homo sapiens.
XX WO9532221-A2.
PN
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US06613.
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krutzch J, Liotta L, Murata J, Schiffmann E, Stracke M;
PI
XX WPI; 1996-020533/02.
DR
XX
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
PT
XX
PS Claim 4; Page 91-94; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
CC sequence represents the full length protein sequence of the A2058
CC melanoma cell line ATX protein. ATX is an autocrine motility
CC stimulating protein which is present in cancer cells. ATX stimulates
CC both random and directed migration of melanoma cells. The tumorous form
CC of ATX is a secreted protein, while the transmembrane bound form is not
CC present in tumour cells. The cDNA encoding this sequence can be used in
CC a vector, to transform cells. The recombinant cells can then be used to
CC produce the peptide sequences. Antibodies specific for these sequences
CC can be produced, and can be used in cancer diagnosis and therapy.

CC Different sites of localisation of the protein are utilised for diagnosis
CC and prognosis of the stages of tumour progression. The sequences can be
CC used in treatment methods to advantageously block the activity of the
CC secreted form of AXT, while having little effect on the membrane form of
CC AXT.
XX
SQ Sequence 915 AA;

Query Match 100.0%; Score 76; DB 17; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | |
Db 201 ymrpvpyptktfpn 213

RESULT 13
AAY71987
ID AAY71987 standard; Protein; 915 AA.
XX
AC AAY71987;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human melanoma autotaxin.
XX
KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; melanoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 127..129
FT /label= RGD_binding_domain
FT Active-site 201..213
FT /note= "Autotaxin phosphodiesterase catalytic site"
XX
PN WO200068386-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12402.
XX
PR 07-MAY-1999; 99US-0306979.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Claim 27; Page 105-108; 126pp; English.
XX
CC The present sequence is autotaxin isolated from human melanoma
CC cells. Autotaxin is a glycoprotein cytokine which increases
CC insulin signalling in adipose tissue by producing substrate for
CC adenosine receptors, resulting in inhibition of lipolysis,
CC decreased hepatic gluconeogenesis and serum glucose levels, and
CC increased insulin sensitivity. It also inhibits differentiation
CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
CC Autotaxin and its analogues are used to stimulate glucose uptake
CC by cells, particularly to reduce serum glucose levels for
CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
CC

CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.
XX Sequence 915 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YMRPVYPTKTFPN 13
Db 201 ymrpvptktpn 213
RESULT 14
AAR86580
ID AAR86580 standard; Protein; 979 AA.
XX
AC AAR86580;
XX
XX 28-JUN-1996 (first entry)
XX Autotaxin derived from human liver cells.
DE
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 864 /note= "unspecified amino acid"
FT
FT Misc-difference 889 /note= "unspecified amino acid"
FT
FT Misc-difference 905 /note= "unspecified amino acid"
FT
FT Misc-difference 911 /note= "unspecified amino acid"
FT
FT Misc-difference 927 /note= "unspecified amino acid"
FT
FT Misc-difference 937 /note= "unspecified amino acid"
FT
FT Misc-difference 944 /note= "unspecified amino acid"
FT
FT Misc-difference 950 /note= "unspecified amino acid"
FT
FT Misc-difference 954 /note= "unspecified amino acid"
FT
FT Misc-difference 967 /note= "unspecified amino acid"
FT
FT Misc-difference 975 /note= "unspecified amino acid"
FT
XX WO9532221-A2.
PN
XX 30-NOV-1995.
PD
XX
XX 24-MAY-1995; 95WO-US06613.
PF
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
PI
XX WPI; 1996-020533/02.
DR
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy

XX Claim 4; Page 67-70; 112pp; English.
PS
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of AXT, while
CC having little effect on the membrane form of AXT.
XX
SQ Sequence 979 AA;
Query Match 100.0%; Score 76; DB 17; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YMRPVYPTKTFPN 13
Db 201 ymrpvptktpn 213
RESULT 15
AAR86595
ID AAR86595 standard; Protein; 849 AA.
XX
AC AAR86595;
XX
XX 01-JUL-1996 (first entry)
DT
XX
DE N-tera 2D1 autotaxin protein.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX Homo sapiens.
OS
XX WO9532221-A2.
PN
XX 30-NOV-1995.
PD
XX
XX 24-MAY-1995; 95WO-US06613.
PF
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
PI
XX WPI; 1996-020533/02.
DR
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
XX
XX Claim 4; Page 86-89; 112pp; English.
PS
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
CC sequence represents the full length protein sequence of the
CC teratocarcinoma N-tera 2D1 ATX protein. ATX is an autocrine motility
CC stimulating protein which is present in cancer cells. ATX stimulates
CC both random and directed migration of melanoma cells. The tumorous
CC form of ATX is a secreted protein, while the transmembrane bound form is
CC not present in tumour cells. The cDNA encoding this sequence can be used
CC in a vector, to transform cells. The recombinant cells can then be used
CC to produce the peptide sequences. Antibodies specific for these

CC sequences can be produced, and can be used in cancer diagnosis and
CC therapy. Different sites of localisation of the protein are utilised for
CC diagnosis and prognosis of the stages of tumour progression. The
CC sequences can be used in treatment methods to advantageously block the
CC activity of the secreted form of AXT, while having little effect on the
CC membrane form of AXT.

XX

SQ Sequence 849 AA;

Query Match 93.4%; Score 71; DB 17; Length 849;
Best Local Similarity 92.3%; Pred. No. 0.00091;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

:|||||

Db 201 hmrpvpyptktfpn 213

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:54 ; Search time 25.97 Seconds
(without alignments)
38.131 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	915	1 A55144	autotaxin precursor
2	70	92.1	885	1 A55453	plasma cell membra
3	69	90.8	96	2 A25274	phosphodiesterase
4	69	90.8	300	2 A41179	protein kinase PC-
5	69	90.8	925	1 A39216	plasma cell membra
6	66	86.8	905	1 A27410	plasma cell membra
7	65	85.5	875	1 A57080	cell surface antig
8	54	71.1	493	2 S50443	hypothetical prote
9	50	65.8	743	2 S19437	hypothetical prote
10	49	64.5	457	2 T09932	nucleotide pyropho
11	49	64.5	461	2 T09933	nucleotide pyropho
12	49	64.5	829	2 T19494	hypothetical prote
13	48	63.2	496	2 T09931	nucleotide pyropho
14	47	61.8	479	2 T03293	nucleotide pyropho
15	45	59.2	674	2 T19495	hypothetical prote
16	44.5	58.6	316	2 S46237	glucan endo-1,3-be
17	42	55.3	429	2 T33724	hypothetical prote
18	41	53.9	247	2 T32514	hypothetical prote
19	41	53.9	381	2 T23250	hypothetical prote
20	41	53.9	427	2 S57776	cysteine proteinas
21	41	53.9	433	2 B82537	phosphodiesterase-
22	41	53.9	493	2 T01206	cysteine proteinas
23	41	53.9	1829	2 T24583	hypothetical prote
24	40	52.6	174	2 S15391	crustacyanin chain
25	40	52.6	205	2 G01942	mitotic feedback c
26	40	52.6	247	2 T45847	hypothetical prote
27	40	52.6	346	2 JA0159	cysteine proteinas
28	40	52.6	466	2 T06416	cysteine proteinas
29	40	52.6	1547	2 JQ0096	hypothetical 176K

30 39 51.3 269 2 A84841 probable embryo-ab
31 39 51.3 321 2 E86423 hypothetical prote
32 39 51.3 453 2 T16795 hypothetical prote
33 39 51.3 471 2 G69809 aminoacid carrier
34 39 51.3 485 2 T40657 probable phophodie
35 39 51.3 528 2 F64580 hypothetical prote
36 39 51.3 528 2 F71931 outer membrane pro
37 39 51.3 1064 2 S52687 serine/threonine-s
38 38 50.0 256 2 T49254 Myb DNA binding pr
39 38 50.0 453 2 S67089 hypothetical prote
40 38 50.0 567 2 C72698 hypothetical prote
41 38 50.0 604 2 S24760 hydroxymethylgluta
42 38 50.0 708 2 T48022 hypothetical prote
43 38 50.0 791 2 T39924 hypothetical prote
44 38 50.0 1068 2 E81965 probable outer mem
45 38 50.0 1082 2 H81020 serotype-1-specifi

ALIGNMENTS

RESULT 1
A55144
autotaxin precursor - human
N;Contains: phosphodiesterase I (EC 3.1.4.1)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55144; A42329
R;Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A;Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A;Reference number: A55144; MUID:95074054
A;Accession: A55144
A;Molecule type: mRNA
A;Residues: 1-915 <MUR>
A;Cross-references: GB:L35594; NID:G537905; PIDN:AAA64785.1; PID:G537906
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cloce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A;Title: Identification, purification, and partial sequence analysis of autotaxin, a
A;Reference number: A42329; MUID:92129337
A;Accession: A42329
A;Molecule type: protein
A;Residues: 256-266;422-444;504-507,'AN';510,'X',511-515;533-548;'S',554-559,'N',561-
A;Experimental source: A2058 melanoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A;Note: a peptide fragment Tyr-Asp-Val-Pro-Trip-Asn-Glu-Thr-Ile was also found
C;Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C;Genetics:
A;Gene: GDB:ATX
A;Cross-references: GDB:378346
A;Map position: 8q22-8qter
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F;55-98/Domain: somatomedin B homology <SBH1>
F;99-142/Domain: somatomedin B homology <SBH2>
F;54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 100.0%; Score 76; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 201 YMRPVYPTKTFPN 213

RESULT 2
A55453
plasma cell membrane glycoprotein PC-1, brain specific - rat
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A55453; JU0187
R;Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
J. Biol. Chem. 269, 28235-28242, 1994
A;Title: Molecular cloning, expression, and localization of a brain-specific phosphodies
A;Reference number: A55453; MUID:95050605
A;Accession: A55453
A;Molecule type: mRNA
A;Residues: 1-885 <NAR>
A;Cross-references: GB:D28560; NID:g464196; PIDN:BAA05910.1; PID:g464197
R;Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994
A;Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase.
A;Reference number: JU0187
A;Accession: JU0187
A;Molecule type: mRNA
A;Residues: 1-66,'Q',68-81,'T',83-94,'C',96,'A',98-195,'A',197-514,'E',516-621,'E',623-6
A;Experimental source: strain Sprague-Dawley
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester hy
F;54-97/Domain: somatomedin B homology <SBH1>
F;98-141/Domain: somatomedin B homology <SBH2>
F;53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status predict
F;207/Binding site: AMP (Thr) (covalent). #status predicted

Query Match 92.1%; Score 70; DB 1; Length 885;
Best Local Similarity 92.3%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
I | | | | | | | | | |
DB 198 YTRPVYPTKTFPN 210

RESULT 3
A25274
phosphodiesterase I (EC 3.1.4.1) - bovine (fragments)
N;Alternate names: 5'-exonuclease
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1988 #sequence_revision 23-Mar-1995 #text_change 21-May-1999
C;Accession: A25274; C48395; A48395; D48395
R;Culp, J.S.; Blytt, H.J.; Hermodson, M.; Butler, L.G.
J. Biol. Chem. 260, 8320-8324, 1985
A;Title: Amino acid sequence of the active site peptide of bovine intestinal 5'-nucleoti
A;Reference number: A25274; MUID:85234541
A;Accession: A25274
A;Molecule type: protein
A;Residues: 1-61 <CUL>
R;Maruyama, E.; Iwamatsu, A.; Takashima, S.
Biochem. Mol. Biol. Int. 29, 579-586, 1993
A;Title: Purification and amino acid microsequencing of alkaline phosphodiesterase I fr
A;Reference number: A48395; MUID:93250579
A;Accession: C48395
A;Molecule type: protein
A;Residues: 22-36;62-73;74-81;82-96 <MAR>
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:132415, NCBIP:131478)
A;Note: the correct order of the fragments is unknown
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: phosphoprotein; phosphoric diester hydrolase
F;39/Binding site: AMP (Thr) (covalent) #status experimental

Query Match 90.8%; Score 69; DB 2; Length 96;
Best Local Similarity 84.6%; Pred. No. 9.1e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
I | | | | | | | | | |
DB 30 YLRPAYPTKTFPN 42

RESULT 4
A41179
protein kinase PC-1 (EC 2.7.1.1) - bovine (fragments)
N;Alternate names: MAFP; major acidic fibroblast growth factor-stimulated phosphoprot
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
C;Accession: A41179; A49308
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 266, 16791-16795, 1991
A;Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein
A;Reference number: A41179; MUID:91358477
A;Accession: A41179
A;Molecule type: protein
A;Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <ODA>
A;Experimental source: liver
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 268, 27318-27326, 1993
A;Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein f
estrase activities.
A;Reference number: A49308; MUID:94086550
A;Accession: A49308
A;Molecule type: protein
A;Residues: 27-35,'X',37-58 <OD2>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:141583)
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: glycoprotein; phosphoprotein; phosphotransferase
F;1-25/Domain: somatomedin B homology (fragment) <SBH>
F;36/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
I | | | | | | | | | |
DB 28 MRPVYPTKTFPN 39

RESULT 5
A39216
plasma cell membrane glycoprotein PC-1 - human
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A39216; S21706; S23587; S51030
R;Buckley, M.F.; Loveland, K.A.; McKinsty, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A;Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
A;Reference number: A39216; MUID:91009202
A;Accession: A39216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-925 <BUC>
A;Cross-references: GB:J05654
R;Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A;Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
A;Reference number: S21706; MUID:92246539
A;Accession: S21706
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-925 <FUN1>
A;Accession: S23587
A;Molecule type: protein
A;Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364;449-465;4

A;Note: it is uncertain whether Met-1 or Met-53 is the initiator
R;Belli, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A;Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph

A;Reference number: S51030; MUID:95094801
A;Accession: S51030
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-80 <BEL>
C;Genetics:

A;Gene: GDB:PDNP1; M6S1; NPPS
A;Cross-references: GDB:132615; OMIM:173335
A;Map position: 6q22-6q23

C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; tran
F;77-97/Domain: transmembrane #status predicted <TMM>
F;104-144/Domain: somatomedin B homology <SBH1>
F;145-188/Domain: somatomedin B homology <SBH2>
F;179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) #s
F;256/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 1; Length 925;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
|||||
Db 248 MRPVYPTKTFPN 259

RESULT 6
A27410

plasma cell membrane glycoprotein PC-1 - mouse
N;Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A27410; I59055; S38354
R;van Driel, I.R.; Goding, J.W.
J. Biol. Chem. 262, 4882-4887, 1987
A;Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA clo
A;Reference number: A27410; MUID:87165906
A;Accession: A27410

A;Molecule type: mRNA
A;Residues: 1-905 <VAN>

A;Cross-references: GB:J02700; NID:g200236; PIDN:AAA39893.1; PID:g200237
A;Note: the authors translated the codon CAG for residue 24 as Glu
R;van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985

A;Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysi
A;Reference number: I59055; MUID:86094275

A;Accession: I59055

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 203-219 <RES>

A;Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235

R;Belli, S.I.; van Driel, I.R.; Goding, J.W.

Eur. J. Biochem. 217, 421-428, 1993

A;Title: Identification and characterization of a soluble form of the plasma cell membra
A;Reference number: S38354; MUID:94039066

A;Accession: S38354

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 35-219 <BEL>

A;Cross-references: EMBL:L04516

C;Genetics:

A;Introns: 62/3; 87/1; 126/1; 168/1; 188/2

C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology

C;Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; tran
F;86-126/Domain: somatomedin B homology <SBH1>

F;127-170/Domain: somatomedin B homology <SBH2>

F;161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;238/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 86.8%; Score 66; DB 1; Length 905;
Best Local Similarity 91.7%; Pred. No. 0.0028;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
|||||
Db 230 MRPVYPTKTFPN 241

RESULT 7
A57080

cell surface antigen RB13-6 - rat
N;Contains: phosphodiesterase I (EC 3.1.4.1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A57080
R;Deissler, H.; Lottspeich, F.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A;Title: Affinity purification and cDNA cloning of rat neural differentiation and tum
A;Reference number: A57080; MUID:95247775
A;Accession: A57080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-875 <DEI>

A;Cross-references: GB:Z47987; NID:g806378; PIDN:CAA88029.1; PID:g806379

C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology

C;Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase;
F;1-22/Domain: cytosolic #status predicted <CYT>

F;23-45/Domain: transmembrane #status predicted <TMM>

F;46-875/Domain: extracellular #status predicted <EXT>

F;51-94/Domain: somatomedin B homology <SBH>

F;95-138/Domain: somatomedin B homology <SBH2>

F;206/Binding site: AMP (Thr) (covalent) #status predicted

F;237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 85.5%; Score 65; DB 1; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0041;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 197 YMRAMYPTKTFPN 209

RESULT 8
S50443

hypothetical protein YEL016c - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999

C;Accession: S50443

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 a

A;Reference number: S50428

A;Accession: S50443

A;Molecule type: DNA

A;Residues: 1-493 <DIE>

A;Cross-references: EMBL:U18530; NID:g602367; PID:g602383; GSPDB:GN00005; MIPS:YEL016

C;Genetics:

A;Gene: MIPS:YEL016c

A;Map position: 5L

Query Match 71.1%; Score 54; DB 2; Length 493;
Best Local Similarity 69.2%; Pred. No. 0.17;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 118 YMIPSFPTQTFPN 130

RESULT 9
SL9437

hypothetical protein YCR026c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCR247
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Dec-1997
C;Accession: S19437; S19750; S27380
R;Pohl, F.; Richterich, P.; Wurst, H.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19437
A;Accession: S19437
A;Molecule type: DNA
A;Residues: 1-244 <POH>
A;Cross-references: EMBL:X59720; MIPS:YCR026c
R;Berben, G.; Bolle, P.A.; Gilliquet, V.; Hilger, F.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19433
A;Accession: S19750
A;Molecule type: DNA
A;Residues: 244-743 <BER>
A;Cross-references: EMBL:X59720; MIPS:YCR026c
R;Bolle, P.A.; Gilliquet, V.; Berben, G.; Dumont, J.; Hilger, F.
Yeast 8, 205-213, 1992
A;Title: The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chromosome 1
A;Reference number: S22273; MUID:92245758
A;Accession: S27380
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-106, 'H', 108-119, 'F', 121-211, 'V', 213-743 <BOL>
C;Genetics:
A;Map position: 3R
C;Keywords: transmembrane protein

Query Match 65.8%; Score 50; DB 2; Length 743;
Best Local Similarity 61.5%; Pred. No. 1.2;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
: | | : || : || || |
Db 210 FMIPSFPTETFPN 222

RESULT 10
T09932
nucleotide pyrophosphatase homolog T16L4.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T09932
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16897
A;Accession: T09932
A;Molecule type: DNA
A;Residues: 1-457 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.200
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.200
A;Map position: 4

Query Match 64.5%; Score 49; DB 2; Length 457;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
| | | | |
Db 94 PVFPTMTFPN 103

RESULT 11
T09933
nucleotide pyrophosphatase homolog T16L4.210 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T09933
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16897
A;Accession: T09933
A;Molecule type: DNA
A;Residues: 1-461 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.210
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.210
A;Map position: 4

Query Match 64.5%; Score 49; DB 2; Length 461;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
| | | | |
Db 97 PVFPTMTFPN 106

RESULT 12
T19494
hypothetical protein C27A7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19494
R;Harris, B.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19132
A;Accession: T19494
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-829 <WIL>
A;Cross-references: EMBL:Z81041; PIDN:CAB02784.1; GSPDB:GN00023; CESP:C27A7.1
A;Experimental source: clone C27A7
C;Genetics:
A;Gene: CESP:C27A7.1
A;Map position: 5
A;Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;

Query Match 64.5%; Score 49; DB 2; Length 829;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
| | | | |
Db 218 PSYPSKTFPN 227

RESULT 13
T09931
nucleotide pyrophosphatase homolog T16L4.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T09931
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16897
A;Accession: T09931
A;Molecule type: DNA
A;Residues: 1-496 <BEV>
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.190
A;Map position: 4

Query Match 63.2%; Score 48; DB 2; Length 496;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13

|||||

Db 146 PVFPTLTFPN 155

RESULT 14

T03293

nucleotide pyrophosphatase homolog - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: T03293

R;Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.

submitted to the EMBL Data Library, April 1995

A;Description: Rice early embryogenesis gene.

A;Reference number: Z14889

A;Accession: T03293

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-479 <HSI>

A;Cross-references: EMBL:U25430; NID:g818848; PID:g818849

A;Experimental source: strain Tainung 67

C;Genetics:

A;Note: OSE4

Query Match 61.8%; Score 47; DB 2; Length 479;
Best Local Similarity 70.0%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13

|||||

Db 129 PIFPTLTFPN 138

RESULT 15

T19495

hypothetical protein C27A7.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T19495

R;Harris, B.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19132

A;Accession: T19495

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-674 <WIL>

A;Cross-references: EMBL:Z81041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3

A;Experimental source: clone C27A7

C;Genetics:

A;Gene: CESP:C27A7.3

A;Map position: 5

A;Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1

Query Match 59.2%; Score 45; DB 2; Length 674;
Best Local Similarity 70.0%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13

|||||

Db 166 PSFPSKTFPN 175

Search completed: July 19, 2001, 14:45:55
Job time: 153 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:47:09 ; Search time 16.91 Seconds
(without alignments)
26.335 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	69	90.8	61	1	PPD1_BOVIN	P15396 bos taurus
2	69	90.8	873	1	PC1_HUMAN	P22413 homo sapien
3	66	86.8	871	1	PC1_MOUSE	P06802 mus musculus
4	54	71.1	493	1	YEB6_YEAST	P39997 saccharomyc
5	50	65.8	743	1	YCR6_YEAST	P25353 saccharomyc
6	44.5	58.6	316	1	E13E_HORVU	Q02438 hordeum vul
7	42	55.3	743	1	BGAL_THEET	P77989 thermoanaer
8	40	52.6	174	1	CRA2_HOMGA	P80007 homarus gam
9	40	52.6	205	1	MD21_HUMAN	Q13257 homo sapien
10	40	52.6	205	1	MD21_MOUSE	Q921b5 mus musculus
11	40	52.6	346	1	CYSL_LYCES	P20721 lycopersico
12	40	52.6	1547	1	RRPO_PMV	P20951 papaya mosa
13	39	51.3	595	1	HMD2_SOLTU	Q41437 solanum tub
14	39	51.3	890	1	YCF2_MESVI	Q9mup8 mesostigma
15	39	51.3	1064	1	KIN1_YEAST	P13185 saccharomyc
16	38	50.0	172	1	CH18_DROME	P07184 drosophila
17	38	50.0	604	1	HMDH_NICSY	Q01559 nicotiana s
18	37	48.7	177	1	CRAB_SQUAC	P02512 squalus aca
19	37	48.7	232	1	HB23_MOUSE	P04231 mus musculus
20	37	48.7	264	1	HB21_MOUSE	P01915 mus musculus
21	37	48.7	264	1	HB22_MOUSE	P20040 mus musculus
22	37	48.7	264	1	HB24_MOUSE	P18468 mus musculus
23	37	48.7	264	1	HB21_MOUSE	P18469 mus musculus
24	37	48.7	264	1	HB2J_MOUSE	P39465 sulfolobus
25	37	48.7	328	1	GPT_SULAC	P21033 vaccinia vi
26	37	48.7	333	1	PAP2_VACCC	P07617 vaccinia vi
27	37	48.7	333	1	PAP2_VARV	P33052 variola vir
28	37	48.7	333	1	PAP2_METJA	Q57911 methanococc
29	37	48.7	480	1	SYFA_METJA	P52488 saccharomyc
30	37	48.7	602	1	HMD2_LYCES	P48022 lycopersico
31	37	48.7	636	1	UBA2_YEAST	Q62059 mus musculus
32	37	48.7	3358	1	PGCV_MOUSE	P55200 mus musculus
33	37	48.7	3866	1	HRX_MOUSE	

34	37	48.7	3969	1	HRX_HUMAN	Q03164 homo sapien
35	36.5	48.0	910	1	SC15_YEAST	P22224 saccharomyc
36	36	47.4	210	1	THIE_ARCFU	O28205 archaeoglob
37	36	47.4	305	1	GP7D_CHLTR	P10561 chlamydia t
38	36	47.4	716	1	BGAL_THETU	P26257 thermoanaer
39	36	47.4	750	1	FOH1_HUMAN	Q04609 homo sapien
40	35.5	46.7	863	1	APCE_CYACA	P35911 cyanidium c
41	35.5	46.7	883	1	APCE_CYAPA	P48088 cyanophora
42	35	46.1	222	1	THIE_BACSU	P39594 bacillus su
43	35	46.1	278	1	TONB_NEIMC	P95374 neisseria m
44	35	46.1	280	1	TONB_NEIMA	P57003 neisseria m
45	35	46.1	280	1	TONB_NEIMB	P57004 neisseria m

ALIGNMENTS

RESULT 1
PPD1_BOVIN
ID PPD1_BOVIN STANDARD; PRT; 61 AA.
AC P15396;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE
DE PHOSPHODIESTERASE) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=85234541; PubMed=2989287;
RA Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;
RT "Amino acid sequence of the active site peptide of bovine intestinal
RT 5'-nucleotide phosphodiesterase and identification of the active
RT site residue as threonine.";
RL J. Biol. Chem. 260:8320-8324(1985).
CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
DR PIR; A25274; A25274.
KW Hydrolase.
FT NON_TER 1 1
FT ACT_SITE 39 39 FORMS A PHOSPHOTHREONINE INTERMEDIATE.
SQ SEQUENCE 61 AA; 6999 MW; 580C8B4807A61C84 CRC64;

Query Match 90.8%; Score 69; DB 1; Length 61;
Best Local Similarity 84.6%; Pred. No. 1.9e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13.
|:|:| | | | | | | | | |
Db 30 YLRPAYPTKTFPN 42

RESULT 2
PC1_HUMAN
ID PC1_HUMAN STANDARD; PRT; 873 AA.
AC P22413; Q9Y6K3; Q9UP61;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
DE (EC 3.6.1.9) (NPPASE)].
GN PDNP1 OR PC1 OR NPPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=91009202; PubMed=2211644;
Buckley M.F., Loveland K.A., McKinsty W.J., Garson O.M., Goding J.W.;
"Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
molecule, amino acid sequence, and chromosomal location.";
J. Biol. Chem. 265:17506-17511(1990).
[2]
SEQUENCE FROM N.A.
MEDLINE=92246539; PubMed=1315502;
Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
Yamashina I.;
"Molecular cloning of cDNAs for human fibroblast nucleotide
pyrophosphatase.";
Arch. Biochem. Biophys. 295:180-187(1992).
[3]
SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
MEDLINE=99408501; PubMed=10480624;
Pizzuti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
Tassi V., Trischitta V.;
"A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
region is strongly associated with insulin resistance.";
Diabetes 48:1881-1884(1999).
CC -1- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
OLIGO-NUCLEOTIDES.
CC -1- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
CC -1- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M57736; AAA63237.1; -.
DR EMBL; D12485; BAA02054.1; -.
DR EMBL; D12485; BAA02053.1; ALT_INIT.
DR EMBL; AF067177; AAD38420.1; -.
DR EMBL; AF067178; AAD38421.1; -.
DR PIR; A39216; A39216.
DR MIM; 173335; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01663; Phosphodiester; 1.
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase;
KW Polymorphism.
FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 46 873 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

```

FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 696 696 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 121 121 K -> Q.
FT SEQUENCE 873 AA; 99929 MW; 872808C20B048070 CRC64; /FTId=VAR_008873.
SQ
Query Match 90.8%; Score 69; DB 1; Length 873;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVPTKTFPN 13
    | | | | | | | | | |
DB 196 MRPVPTKTFPN 207

RESULT 3
PCL_MOUSE
ID PCL_MOUSE STANDARD; PRT; 871 AA.
AC P06802;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
DE (EC 3.6.1.9) (NPPASE)]].
GN PDNP1 OR PC1 OR NPPS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87165906; PubMed=3104326;
RA van Driel I.R., Goding J.W.;
RT "Plasma cell membrane glycoprotein PC-1. Primary structure deduced
RT from cDNA clones.";
RL J. Biol. Chem. 262:4882-4887(1987).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=85056299; PubMed=3917281;
RA Stearne P.A., van Driel I.R., Grego B., Simpson R.J., Goding J.W.;
RT "The murine plasma cell antigen PC-1: purification and partial amino
RT acid sequence.";
RL J. Immunol. 134:443-448(1985).
RN [3]
RP FUNCTION, AND SEQUENCE FROM N.A.
RX MEDLINE=91271356; PubMed=1647027;
RA Rebbe N.F., Tong B.D., Finley E.M., Hickman S.;
RT "Identification of nucleotide pyrophosphatase/alkaline
RT phosphodiesterase I activity associated with the mouse plasma cell
RT differentiation antigen PC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).
RN [4]
RP SEQUENCE OF 169-185 FROM N.A.
RX MEDLINE=86094275; PubMed=3001713;
RA van Driel I.R., Wilks A.F., Pietersz G.A., Goding J.W.;
RT "Murine plasma cell membrane antigen PC-1: molecular cloning of cDNA
RT and analysis of expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623(1985).
CC -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
CC -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF
CC ANTIBODY-SECRETING CELLS.
CC -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation

```

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; J02700; AAA39893.1; ALT_INIT.
EMBL; M12552; AAA39892.1; -
PIR; A27410; A27410.
MGD; MGI:97370; Pdnpl.
InterPro; IPR001212; -
InterPro; IPR002591; -
Pfam; PF01663; Phosphodiester; 1.
Pfam; PF01033; Somatomedin_B; 2.
PRINTS; PR00022; SOMATOMEDINB.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase.
MOD_RES ?1 ?1
DOMAIN 1 24
TRANSMEM 25 45
DOMAIN 46 871
DOMAIN 52 92
DOMAIN 93 136
CARBOHYD 127 127
CARBOHYD 233 233
CARBOHYD 289 289
CARBOHYD 425 425
CARBOHYD 533 533
CARBOHYD 590 590
SEQUENCE 871 AA; 99487 MW; 80848F81071F70AA CRC64;

Query Match 86.8%; Score 66; DB 1; Length 871;
Best Local Similarity 91.7%; Pred. No. 0.001;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
|||:|||||
DB 196 MRPVYPTKTFPN 207

RESULT 4
YEB6_YEAST
ID YEB6_YEAST STANDARD; PRT; 493 AA.
AC P39997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
GN YEL016C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: TO YEAST YCR26C.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; U18530; AAB64493.1; -
CC SGD; S0000742; YEL016C.
CC InterPro; IPR002591; -
CC Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 57354 MW; 10E67A05C6DEDF09 CRC64;

Query Match 71.1%; Score 54; DB 1; Length 493;
Best Local Similarity 69.2%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||:|||||
DB 118 YMRPVYPTKTFPN 130

RESULT 5
YCR6_YEAST
ID YCR6_YEAST STANDARD; PRT; 743 AA.
AC P25353;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 84.9 KDA PROTEIN IN PMP1-FEN2 INTERGENIC REGION.
GN YCR026C OR YCR26C OR YCR246.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-244 FROM N.A.
RA Pohl F., Richterich P., Wurst H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 244-743 FROM N.A.
RX MEDLINE=92245758; PubMed=1574926;
RA Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.;
RT "The complete sequence of K3B, a 7.9 kb fragment between PGK1 and
RT CRY1 on chromosome III, reveals the presence of seven open reading
RT frames."
RL Yeast 8:205-213(1992).
CC -!- SIMILARITY: TO YEAST YEL016C.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X59720; CAA42318.1; -
PIR; S19437; S19437.
PIR; S27380; S27380.
SGD; S0000621; YCR026C.
InterPro; IPR002591; -
Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

Query Match 65.8%; Score 50; DB 1; Length 743;
Best Local Similarity 61.5%; Pred. No. 0.47;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||:|||||
DB 210 FMIPSFPTTFPN 222


```
RESULT 6
E13E_HORVU
ID E13E_HORVU STANDARD; PRT; 316 AA.
AC Q02438;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GV (EC 3.2.1.39) ((1->3)-BETA-GLUCAN
DE ENDOHYDROLASE GV) ((1->3)-BETA-GLUCANASE ISOENZYME GV) (BETA-1,3-
DE ENDOGLUCANASE GV).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
OC Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=94307426; PubMed=8034043;
RA Xu P., Harvey A.J., Fincher G.B.;
RT "Heterologous expression of cDNAs encoding barley (Hordeum vulgare)
RT (1->3)-beta-glucanase isoenzyme GV.";
RL FEBS Lett. 348:206-210(1994).
RN [2]
RP SEQUENCE OF 5-316 FROM N.A.
RC STRAIN=CV. CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=93013030; PubMed=1398132;
RA Xu P., Wang J., Fincher G.B.;
RT "Evolution and differential expression of the (1->3)-beta-glucan
RT endohydrolase-encoding gene family in barley, Hordeum vulgare.";
RL Gene 120:157-165(1992).
CC -!- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
CC INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE
CC FUNGAL CELL WALL POLYSACCHARIDES.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
CC IN 1,3-BETA-D-GLUCANS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
EMBL; M96939; AAA21564.1; -.
DR PIR; JC1438; JC1438.
DR HSP; P15737; IGHS.
DR InterPro; IPR000490; -.
DR Pfam; PF00332; Glyco_hydro_17; 1.
DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolase; Glycosidase; Multigene family.
FT ACT_SITE 239 239 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 296 296 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 316 AA; 34413 MW; 0CC0AA9D48269B4F CRC64;

Query Match 58.6%; Score 44.5; DB 1; Length 316;
Best Local Similarity 81.8%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 RPVYPTKTFPN 13
:|||||
Db 307 QPVYPT-TFPN 316

RESULT 7
BGAL_THEET
ID BGAL_THEET STANDARD; PRT; 743 AA.
AC P77989;

Query Match 55.3%; Score 42; DB 1; Length 743;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
||:||||:|
Db 454 YMGHMYPTKSYDN 466

RESULT 8
CRA2_HOMGA
ID CRA2_HOMGA STANDARD; PRT; 174 AA.
AC P80007;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE CRUSTACYNIN A2 SUBUNIT.
OS Homarus gammarus (European lobster) (Homarus vulgaris).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6707;
RN [1]
RP SEQUENCE.
RX MEDLINE=91224133; PubMed=2026162;
RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F.,
RA Findlay J.B.C.;
RT "Complete sequence and model for the A2 subunit of the carotenoid
RT pigment complex, crustacyanin.";
RL Eur. J. Biochem. 197:407-417(1991).
CC -!- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE
CC COLORATION TO THE CARAPACE OF THE LOBSTER.
CC -!- SUBUNIT: OLIGOMER; CAN FORM DIMERS (BETA-CRUSTACYNIN); OR
CC COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYNIN). THERE ARE FIVE
CC TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.
```

```
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
GN LACZ OR LACA.
OS Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacter.
OX NCBI_TaxID=1757;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33223 / 39E;
RA Zverlov V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
EMBL; Y08557; CAA69850.1; -.
DR InterPro; IPR001649; -.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
KW Hydrolase; Glycosidase.
FT ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 453 453 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 743 AA; 85796 MW; FE011FF517E51DFC CRC64;

Query Match 55.3%; Score 42; DB 1; Length 743;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
||:||||:|
Db 454 YMGHMYPTKSYDN 466

RESULT 8
CRA2_HOMGA
ID CRA2_HOMGA STANDARD; PRT; 174 AA.
AC P80007;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE CRUSTACYNIN A2 SUBUNIT.
OS Homarus gammarus (European lobster) (Homarus vulgaris).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6707;
RN [1]
RP SEQUENCE.
RX MEDLINE=91224133; PubMed=2026162;
RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F.,
RA Findlay J.B.C.;
RT "Complete sequence and model for the A2 subunit of the carotenoid
RT pigment complex, crustacyanin.";
RL Eur. J. Biochem. 197:407-417(1991).
CC -!- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE
CC COLORATION TO THE CARAPACE OF THE LOBSTER.
CC -!- SUBUNIT: OLIGOMER; CAN FORM DIMERS (BETA-CRUSTACYNIN); OR
CC COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYNIN). THERE ARE FIVE
CC TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.
```


CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
DR PIR; S15391; S15391.
DR InterPro; IPR000566; -.
DR InterPro; IPR002345; -.
DR InterPro; IPR003057; -.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PRINTS; PR01273; INVTBRTCOLOR.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Pigment; Lipocalin; Transport.
FT DISULFID 12 119 BY SIMILARITY.
FT DISULFID 46 170 BY SIMILARITY.
SQ SEQUENCE 174 AA; 19670 MW; AC47FAA650C5E44E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 174;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VYPTKTEP 12
|||||
Db 80 VYPTKEFP 87

RESULT 9
MD21_HUMAN STANDARD; PRT; 205 AA.
ID MD21_HUMAN
AC Q13257;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1)
DE (HSMAD2).
GN MAD2L1 OR MAD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421709; PubMed=8824189;
RA Li Y., Benezra R.;
RT "Identification of a human mitotic checkpoint gene: hSMAD2.";
RL Science 274:246-248(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Jin D.-Y., Jeang K.-T.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kleibert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP INTERACTION WITH CDC20.
RX MEDLINE=98301442; PubMed=9637688;
RA Fang G., Yu H., Kirschner M.W.;
RT "The checkpoint protein MAD2 and the mitotic regulator CDC20 form a
RT ternary complex with the anaphase-promoting complex to control
RT anaphase initiation.";
RL Genes Dev. 12:1871-1883(1998).
RN [5]
RP INTERACTION WITH ADAM17.
RX PubMed=10527948;
RA Nelson K.K., Schlondorff J., Blobel C.P.;
RT "Evidence for an interaction of the metalloprotease-disintegrin tumour
RT necrosis factor alpha convertase (TACE) with mitotic arrest deficient
RT 2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel
RT MAD2-related protein, MAD2-beta.";
RL Biochem. J. 343:673-680(1999).
RN [6]
RP STRUCTURE BY NMR OF 11-195.
RX MEDLINE=20165182; PubMed=10700282;
RA Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,

Wagner G.;
"Structure of the Mad2 spindle assembly checkpoint protein and its
interaction with Cdc20.";
Nat. Struct. Biol. 7:224-229(2000).
CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
CC WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND
CC DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE.
CC -!- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U65410; AAC50781.1; -.
DR EMBL; U31278; AAC52060.1; -.
DR EMBL; AJ000186; CAA03943.1; -.
DR MIM; 601467; -.
DR PDB; 1DUJ; 08-MAR-00.
DR InterPro; IPR003511; -.
DR Pfam; PF02301; HORMA; 1.
KW Cell cycle; Mitosis; Nuclear protein; 3D-structure.
SQ SEQUENCE 205 AA; 23510 MW; B8DCBF0043836764 CRC64;
Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 YMRPVYPTKTF 11
| | :| :| :|
Db 33 YQGIYPSETF 43
RESULT 10
MD21_MOUSE STANDARD; PRT; 205 AA.
ID MD21_MOUSE
AC Q9Z1B5; Q9JI53;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1).
GN MAD2L1 OR MAD2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Jin D.-Y., Jeang K.-T.;
RT "Identification of a novel component of the spindle assembly
RT checkpoint in mammalian cells.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX PubMed=10892650;
RA Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
RT "Chromosome missegregation and apoptosis in mice lacking the mitotic
RT checkpoint protein Mad2.";
RL Cell 101:635-645(2000).
CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
CC WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND
CC DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT

CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE (BY SIMILARITY).
CC
CC -!- SUBUNIT: INTERACTS WITH CDC20.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U83902; AAD09238.1; -.
CC DR EMBL; AF261919; AAF69525.1; -.
CC DR InterPro; IPR003511; -.
CC DR Pfam; PF02301; HORMA; 1.
CC KW Cell cycle; Mitosis; Nuclear protein.
CC FT CONFLICT 157 157 T -> A (IN REF. 1).
CC FT CONFLICT 178 178 C -> S (IN REF. 1).
CC FT CONFLICT 201 201 T -> I (IN REF. 1).
CC SQ SEQUENCE 205 AA; 23598 MW; A9F3F28BC4C9738E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTF 11
| | :||:|
Db 33 YQGIYPSETF 43

RESULT 11
CYSL_LYCES
ID CYSL_LYCES STANDARD; PRT; 346 AA.
AC P20721;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOW-TEMPERATURE-INDUCED CYSTEINE PROTEINASE PRECURSOR (EC 3.4.22.-)
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY;
RA Schaffer M.A., Fischer R.L.;
RT "Analysis of mRNAs that accumulate in response to low temperature
RT identifies a thiolprotease in tomato."
RL Plant Physiol. 87:431-436(1988).
CC -!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAIN FAMILY OF THIOL PROTEASES.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M21444; AAA66308.1; -.
CC DR PIR; JA0159; JA0159.
CC DR HSSP; P00785; 2ACT.
CC DR MEROPS; C01.029; -.
CC DR InterPro; IPR000118; -.
CC

DR InterPro; IPR000169; -.
DR InterPro; IPR000668; -.
DR Pfam; PF00112; Peptidase_C1; 1.
DR Pfam; PF00396; granulin; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
KW Hydrolase; Thiol protease; Zymogen; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 17 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 18 346 LOW-TEMPERATURE-INDUCED CYSTEINE
FT PROTEINASE.
FT ACT_SITE 42 42 BY SIMILARITY.
FT ACT_SITE 178 178 BY SIMILARITY.
FT ACT_SITE 198 198 BY SIMILARITY.
FT DISULFID 39 81 BY SIMILARITY.
FT DISULFID 73 114 BY SIMILARITY.
FT DISULFID 172 223 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 346 AA; 37429 MW; D42AC73944010928 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 346;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MRPVYPTKTFPN 13
: | | | | |
Db 227 IEPSYPVKTGPN 238

RESULT 12
RRPO_PMV
ID RRPO_PMV STANDARD; PRT; 1547 AA.
AC P20951;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (176 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DE DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Papaya mosaic potexvirus (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12181;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89381685; PubMed=2778435;
RA Sit T.L., Abouhaidar M.G., Holy S.;
RT "Nucleotide sequence of papaya mosaic virus RNA."
RL J. Gen. Virol. 70:2325-2331(1989).
CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; D13957; BAA03050.1; -.
DR PIR; JQ0096; JQ0096.
DR InterPro; IPR000606; -.
DR Pfam; PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW transferase.
FT NP_BIND 822 829 ATP (POTENTIAL).
SQ SEQUENCE 1547 AA; 176320 MW; 6CA4282C6A082622 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 1547;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPTKTEPN 13
Db 409 YPTKTFDN 416

RESULT 13
HMD2_SOLUTU STANDARD; PRT; 595 AA.
AC Q41437;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (EC 1.1.1.34) (HMG-
COA REDUCTASE 2) (HMG2.2).
GN HMG2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KENNEBEC; TISSUE=Tuber;
RX MEDLINE=97201488; PubMed=9049274;
RA Korth K.L., Stermer B.A., Bhattacharyya M.K., Dixon R.A.;
RT "HMG-CoA reductase gene families that differentially accumulate
transcripts in potato tubers are developmentally expressed in floral
tissues";
RL Plant Mol. Biol. 33:545-551(1997).
CC -!- FUNCTION: CATALYZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC
PRECUSOR OF ALL ISOPRENOID COMPOUNDS PRESENT IN PLANTS.
CC -!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-
HYDROXY-3-METHYLGLUTARYL-COA + 2 NADP.
CC -!- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
RETICULUM.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE
SEEDS AND OVARIES.
CC -!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; U51985; AAB52551.1; -
DR Mendel; 10574; Soltu;1091;10574.
DR InterPro; IPR002202; -
DR Pfam; PF00368; HMG-CoA_red; 1.
DR PRINTS; PR00071; HMGCOARDTASE.
DR PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.
DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; 1.
DR PROSITE; PS01192; HMG_COA_REDUCTASE_3; 1.
DR PROSITE; PS50065; HMG_COA_REDUCTASE_4; 1.
KW Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
KW Isoprene biosynthesis; NADP; Multigene family.
FT DOMAIN 1 112 MEMBRANE-BOUND (BY SIMILARITY).
FT DOMAIN 113 183 LINKER (BY SIMILARITY).
FT DOMAIN 184 595 CATALYTIC (BY SIMILARITY).
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT ACT_SITE 278 278 BY SIMILARITY.
FT ACT_SITE 486 486 BY SIMILARITY.
FT ACT_SITE 584 584 GENERAL BASE (BY SIMILARITY).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 588 588 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 595 AA; 63841 MW; 0FA7069849D41D57 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 595;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPVYPTKTF 11
Db 9 KPVYPSKVF 17

RESULT 14
YCF2_MESVI
ID YCF2_MESVI STANDARD; PRT; 890 AA.
AC Q9MUP8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 103.9 KDA PROTEIN YCF2 (RF2).
GN YCF2.
OS Mesostigma viride.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -!- SIMILARITY: BELONGS THE YCF2 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; AF166114; AAF43852.1; -
DR InterPro; IPR001081; -
DR InterPro; IPR001939; -
DR Pfam; PF00004; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 890 AA; 103935 MW; 43CAEEE991AF2C4B CRC64;

Query Match 51.3%; Score 39; DB 1; Length 890;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPVYPTKTFP 12
Db 650 RPVYSVKLFP 659

RESULT 15
KIN1_YEAST
ID KIN1_YEAST STANDARD; PRT; 1064 AA.
AC P13185; Q04606;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROTEIN KINASE KIN1 (EC 2.7.1.-).
GN KIN1 OR YDR122W OR YD9727.17.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317589; Pubmed=2957690;
RA Levin D.E., Hammond C.I., Ralston R.O., Bishop J.M.;
RT "Two yeast genes that encode unusual protein kinases.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Shore L., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
CC KINASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIM1 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M69017; AAA34722.1; -;
DR EMBL; Z48758; CAA88675.1; -;
DR PIR; S42438; S42438.
DR HSSP; Q63450; 1A06.
DR SGD; S0002529; KIN1.
DR InterPro; IPR000719; -;
DR InterPro; IPR002290; -;
DR Pfam; PF00069; pkkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 120 398 PROTEIN KINASE.
FT NP_BIND 126 134 ATP (BY SIMILARITY).
FT BINDING 149 149 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 BY SIMILARITY.
FT CONFLICT 25 25 S -> R (IN REF. 1).
FT CONFLICT 453 453 T -> H (IN REF. 1).
FT CONFLICT 455 455 V -> G (IN REF. 1).
FT CONFLICT 718 718 A -> R (IN REF. 1).
FT CONFLICT 920 921 NI -> IN (IN REF. 1).
FT CONFLICT 976 976 T -> A (IN REF. 1).
FT CONFLICT 979 980 SI -> T (IN REF. 1).
FT CONFLICT 984 985 KT -> NS (IN REF. 1).
SQ SEQUENCE 1064 AA; 120070 MW; E4104B84A8E45C36 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 1064;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFP 12
||||| |:
Db 802 YMRPPMPSSAYP 813

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:46:48 ; Search time 42.51 Seconds
(without alignments)
40.460 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 segs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL16.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	76	100.0	862	11 Q9R1E6	Q9r1e6 mus musculu
2	76	100.0	863	4 Q13822	Q13822 homo sapien
3	76	100.0	863	4 Q15117	Q15117 homo sapien
4	76	100.0	915	4 Q13827	Q13827 homo sapien
5	70	92.1	885	11 Q64610	Q64610 rattus norv
6	69	90.8	257	11 O88827	O88827 rattus norv
7	69	90.8	845	4 Q9NP23	Q9np23 homo sapien
8	69	90.8	925	4 Q9P1P6	Q9plp6 homo sapien
9	68	89.5	875	11 P97675	P97675 rattus norv
10	68	89.5	876	11 P70641	P70641 rattus norv
11	65	85.5	875	4 O14638	O14638 homo sapien
12	65	85.5	875	11 Q63490	Q63490 rattus norv
13	65	85.5	875	11 P97676	P97676 rattus norv
14	64	84.2	32	6 Q9TRD2	Q9trd2 bos taurus
15	64	84.2	817	14 O90761	O90761 fowlpox vir
16	64	84.2	817	14 Q9J5H1	Q9j5h1 fowlpox vir
17	49	64.5	457	10 Q9SU82	Q9su82 arabidopsis
18	49	64.5	461	10 Q9SU81	Q9su81 arabidopsis
19	49	64.5	829	5 P90754	P90754 caenorhabdi

20	48	63.2	479	10 Q9FS13	Q9fs13 spinacia ol
21	48	63.2	496	10 Q9SU83	Q9su83 arabidopsis
22	47	61.8	479	10 Q42974	Q42974 oryza sativ
23	45	59.2	674	5 P90755	P90755 caenorhabdi
24	43	56.6	173	4 Q9Y5A0	Q9y5a0 homo sapien
25	43	56.6	343	3 Q9UUN9	Q9uun9 sporobolomy
26	43	56.6	401	4 Q9HAC9	Q9hac9 homo sapien
27	43	56.6	757	11 Q9WVC8	Q9wvc8 mus musculu
28	42	55.3	429	2 O69013	O69013 zymomonas m
29	42	55.3	1004	5 Q9V3H9	Q9v3h9 drosophila
30	41	53.9	247	5 O44145	O44145 caenorhabdi
31	41	53.9	381	5 Q9XUV4	Q9xuv4 caenorhabdi
32	41	53.9	427	10 Q43423	Q43423 dianthus ca
33	41	53.9	433	2 Q9PAB9	Q9pab9 xylella fas
34	41	53.9	453	4 Q9Y6X5	Q9y6x5 homo sapien
35	41	53.9	493	10 O22499	O22499 zea mays (m
36	41	53.9	1829	5 Q22248	Q22248 caenorhabdi
37	40	52.6	203	13 P79935	P79935 xenopus lae
38	40	52.6	247	10 Q9SN23	Q9sn23 arabidopsis
39	40	52.6	291	10 Q9M4F6	Q9m4f6 brassica na
40	40	52.6	307	5 O61478	O61478 dreissena p
41	40	52.6	430	5 Q9NB54	Q9nb54 dreissena p
42	40	52.6	466	10 O49877	O49877 lycopersico
43	40	52.6	2066	14 P89920	P89920 oat blue dw
44	40	52.6	3579	5 Q9V5N8	Q9v5n8 drosophila
45	39	51.3	157	5 Q9Y0E8	Q9y0e8 drosophila

ALIGNMENTS

RESULT 1
Q9R1E6
ID Q9R1E6 PRELIMINARY; PRT; 862 AA.
AC Q9R1E6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).
GN NPPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B/6;
RA Sano K., Piao J.-H.;
RT "Cloning and chromosomal assignment of mouse phosphodiesterase
RT I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF123542; AAD46480.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiect; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00201; SO; 1.
KW Hydrolase.
SQ SEQUENCE 862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;

Query Match 100.0%; Score 76; DB 11; Length 862;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|
Db 200 YMRPVYPTKTFPN 212

RESULT 2


```
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE=95050605; PubMed=7961762;
RA Narita M., Goji J., Nakamura H., Sano K.;
RT "Molecular cloning, expression, and localization of a brain-specific
RT phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
RT brain.";
RL J. Biol. Chem. 269:28235-28242(1994).
DR EMBL; D28560; BAA05910.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 885 AA; 101309 MW; 8C5C0AFC52007973 CRC64;

Query Match 92.1%; Score 70; DB 11; Length 885;
Best Local Similarity 92.3%; Pred. No. 0.00065;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 198 YTRPVYPTKTFPN 210

RESULT 6
O88827
ID O88827 PRELIMINARY; PRT; 257 AA.
AC O88827;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PLASMA CELL MEMBRANE GLYCOPROTEIN (FRAGMENT).
GN PCL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakoda H., Asano T., Ogiwara T.;
RT "N terminal of the plasma cell membrane glycoprotein PC-1.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017596; BAA33393.1; -.
DR InterPro; IPR001212; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00201; SO; 1.
FT NON_TER 257
SQ SEQUENCE 257 AA; 28306 MW; CF348E474FBDAFED CRC64;

Query Match 90.8%; Score 69; DB 11; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
Db 230 MRPVYPTKTFPN 241

RESULT 7
Q9NPZ3
ID Q9NPZ3 PRELIMINARY; PRT; 845 AA.
AC Q9NPZ3;
```

```
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DJ131F15.2 (PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE.1
DE (HOMOLOGOUS TO MOUSE LY-41 ANTIGEN) (PCL, NPPS)) (FRAGMENT).
GN PDNPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peck A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117378; CAB99365.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
FT NON_TER 1
SQ SEQUENCE 845 AA; 96844 MW; C2DD58248BDAC52E CRC64;

Query Match 90.8%; Score 69; DB 4; Length 845;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
Db 168 MRPVYPTKTFPN 179

RESULT 8
Q9P1P6
ID Q9P1P6 PRELIMINARY; PRT; 925 AA.
AC Q9P1P6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PDNPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bozzali M., Pizzuti A., Trischitta E.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110304; AAF36094.1; -.
DR EMBL; AF110280; AAF36094.1; JOINED.
DR EMBL; AF110281; AAF36094.1; JOINED.
DR EMBL; AF110283; AAF36094.1; JOINED.
DR EMBL; AF110284; AAF36094.1; JOINED.
DR EMBL; AF110285; AAF36094.1; JOINED.
DR EMBL; AF110286; AAF36094.1; JOINED.
DR EMBL; AF110287; AAF36094.1; JOINED.
DR EMBL; AF110288; AAF36094.1; JOINED.
DR EMBL; AF110289; AAF36094.1; JOINED.
DR EMBL; AF110290; AAF36094.1; JOINED.
DR EMBL; AF110291; AAF36094.1; JOINED.
DR EMBL; AF110292; AAF36094.1; JOINED.
DR EMBL; AF110293; AAF36094.1; JOINED.
DR EMBL; AF110294; AAF36094.1; JOINED.
DR EMBL; AF110295; AAF36094.1; JOINED.
DR EMBL; AF110296; AAF36094.1; JOINED.
DR EMBL; AF110297; AAF36094.1; JOINED.
DR EMBL; AF110298; AAF36094.1; JOINED.
DR EMBL; AF110299; AAF36094.1; JOINED.
DR EMBL; AF110300; AAF36094.1; JOINED.
```

DR EMBL; AF110301; AAF36094.1; JOINED.
DR EMBL; AF110302; AAF36094.1; JOINED.
DR EMBL; AF110303; AAF36094.1; JOINED.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 925 AA; 104924 MW; 0ECAA063801CAFEB CRC64;

Query Match 90.8%; Score 69; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
|||||
Db 248 MRPVYPTKTFPN 259

RESULT 9
P97675
ID P97675 PRELIMINARY; PRT; 875 AA.
AC P97675;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL; U78787; AAB61535.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99166 MW; 8FEB9A482173D377 CRC64;

Query Match 89.5%; Score 68; DB 11; Length 875;
Best Local Similarity 92.3%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 197 YMRVYPTKTFPN 209

RESULT 10
P70641
ID P70641 PRELIMINARY; PRT; 876 AA.
AC P70641;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;
RA Sano K.;
RT "Molecular cloning of phosphodiesterase I cDNA from rat small
RT intestine.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D30649; BAA06333.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 876 AA; 99328 MW; D2F772C34A0C437A CRC64;

Query Match 89.5%; Score 68; DB 11; Length 876;
Best Local Similarity 92.3%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 197 YMRVYPTKTFPN 209

RESULT 11
O14638
ID O14638 PRELIMINARY; PRT; 875 AA.
AC O14638;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)
DE (PHOSPHODIESTERASE I BETA).
GN PDNP3.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=98008933; PubMed=9344668;
RA Piao J.-H., Goding J.W., Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal localization of PD-Ibeta (PDNP3), a
RT new member of the human phosphodiesterase I genes.";
RL Genomics 45:412-415(1997).
RN [2]
RP SEQUENCE OF 189-875 FROM N.A.
RA Hou S., Wohldmann P., Le T.;
RT "The sequence of Homo sapiens PAC clone DJ0988G15.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.H.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.H.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 189-875 FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005632; AAC51813.1; -.
DR EMBL; AC005587; AAD05192.1; -.
DR InterPro; IPR001212; -.
DR

DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 875 AA; 100096 MW; 329CF41667497BC4 CRC64;

Query Match 85.5%; Score 65; DB 4; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 | | | : | | | | | | |
Db 196 YMRAMYPTKTFPN 208

RESULT 12
Q63490
ID Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE RB13-6 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=9524775; PubMed=7730366;
RA Deissler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
and tumor cell surface antigen gpl30RB13-6 reveals relationship to
human and murine PC-1.";
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL; Z47987; CAA88029.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 9BA9FBFFEF82DFBA6 CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 | | | : | | | | | | |
Db 197 YMRAMYPTKTFPN 209

RESULT 13
P97676
ID P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
alkaline phosphodiesterase I expressed on the apical and basolateral
plasma membrane surfaces of rat hepatocytes.";
RT Hepatology 25:995-1002(1997).
RL EMBL; U78788; AAB61536.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 | | | : | | | | | | |
Db 197 YMRAMYPTKTFPN 209

RESULT 14
Q9TRD2
ID Q9TRD2 PRELIMINARY; PRT; 32 AA.
AC Q9TRD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 260 KDA MAJOR ACIDIC FIBROBLAST GROWTH FACTOR-STIMULATED
DE PHOSPHOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94086550; PubMed=7505270;
RA Oda Y., Kuo M.D., Huang S.S., Huang J.S.;
RT "The major acidic fibroblast growth factor (aFGF)-stimulated
phosphoprotein from bovine liver plasma membranes has aFGF-stimulated
kinase, autoadenylylation, and alkaline nucleotide phosphodiesterase
activities.";
RT J. Biol. Chem. 268:27318-27326(1993).
RL J. Biol. Chem. 268:27318-27326(1993).
SQ SEQUENCE 32 AA; 3699 MW; 5CCFFA9EB55E6927 CRC64;

Query Match 84.2%; Score 64; DB 6; Length 32;
Best Local Similarity 91.7%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
 | | | | | | | | | | | | |
Db 2 MRPVYPTKXFPN 13

RESULT 15
O90761
ID O90761 PRELIMINARY; PRT; 817 AA.
AC O90761;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-
NUCLEOTIDE PHOSPHODIESTERASE).
GN PCl.
OS Fowlpox virus.

